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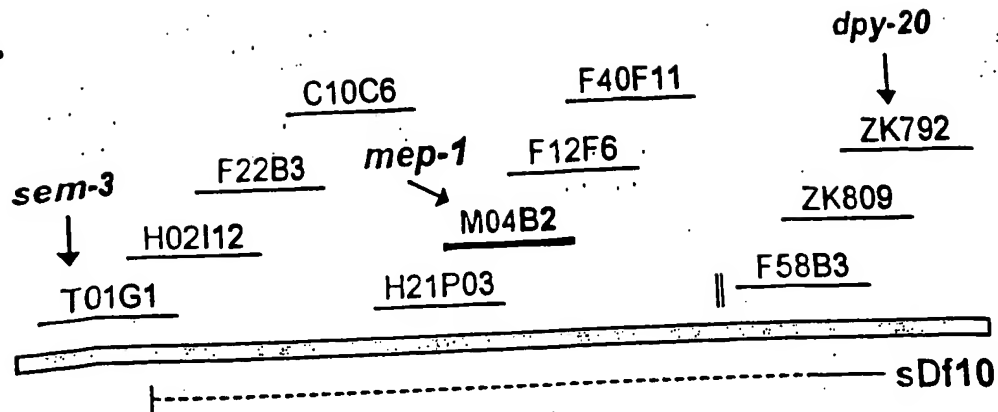
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FIGURE 1

A.



B.

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M V T A D E T V L A T T T N T T S M S V E P T D P R S A G E 30
S S S D S E P D T I E Q L K A E Q R E V M A D A A N G S E V 60
N G N Q E N G K E E A A S A D V E V I E I D D T E E S T D P 90
S P D G S D E N G D A A S T S V P I E E E A R K K D E G A S 120
E V T V A S S E I E Q D D D G D V M E I T E E P N G K S E D 150
T A N G T V T E E V L D E E E P E P S V N G T T E I A T E K 180
E P E D S S M P V E Q N G K G V K R P V E C I E L D D D D D 210
D E I Q E I S T P A P A K K A K I D D V K A T S V P E E D N 240
N E Q A Q K R L L D K L E E Y V K E Q K D Q P S S K S R K V 270
L D T L L G A I N A Q V Q K E P L S V R K L I L D K V L V L 300
P N T I S F P P S Q V C D L L I E H D P E M P L T K V I N R 330
M F G E E R P K L S D S E K R E R A Q L K Q H N P V P N M T 360
K L L V D I G Q D L V Q E A T Y C D I V H A K N L P E V P K 390
N L E T Y K Q V A A Q L K P V W E T L K R K N E P Y K L K M 420
H R G G V G G G G G G G G G G G G G G G G G G G G G G G 450
Q G G G G G G G G G G G G G G G G G G G G G G G G G G G 480
E K E S K Y P C A I C E E D F N F K G V R E Q H Y K Q C K K 510
D Y I R I R N I M M P K Q D D H L Y I N R W L W E R P Q L D 540
P S I L Q Q Q Q Q A A L Q Q A Q Q K K Q Q Q L L H Q Q Q A A 570
Q A A A A A Q L L R K Q Q L Q Q Q Q Q Q Q Q Q A R L R E Q Q Q 600
A A Q F R Q V A Q L L Q Q Q S A Q A Q R A Q Q N Q G N V N H 630
N T L I A A M Q A S L R R G G Q Q G N S L A V S Q L L Q K Q 660
M A A L K S Q Q G A Q Q L Q A A V N S M R S Q N S Q K T P T 690
H R T P T F V G G G G G G G G G G G G G G G G G G G G G G 720
Q M V G K V L Q D M S G G A P L A G S S R G R R D A T L W A T E S 750
L E R H L V M S H G L V T A D L L L K A Q K K E D G G R I C K 780
T G G K N E A T E N M L G H L V A D H Q V K L C S A E I M Y S 810
G D V G A F K G C S S Y G T L E A H L U T S N H P K G D K K T S 840
T P A K K D D C I T L D D 853

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Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE LET-60 RAS SIGNALING

Applicant(s): Horvitz et al.

Filing Date: September 12, 2003 Serial No.: N/A

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FIGURE 2

mep-1 genomic sequence

TCACACACTCATGACATACACACATCATTTTCGCCTCACACACCGCGCCGTCCG
 CCATCCGCACCGCCCGGGTGGGACGTGTTCAAACCTTTTCGGTTTTTCGTAAT
 TAATAGTGAGCCCCGGTTTATTTCGCTTGAGAATCAGTATAATGGATATATC
 AGATTGTGTAATTAGGTTGCGTGCTTGAACCTTTTAAAATTAACGTGTTTTAAAT
 TTATCTGCCTTTATCGTTACAGTAAATCATTTTGATGAACCTTTTCGGATGAAT
 CATAATGAAGTACGCAGCGCTCTAACAAAATGTGTTTGTAAATTCCAATTGC
 TACAAGTTGCCCGGCTTATTTTTGGTGATTGAAGCATGATTCTGTTGACGC
 TCCCGACGCGGAATACCAGGACGGACCGATGAGAGAGTACTGCCAGTGAA
 GAGACGCATGCGAGCAGGACGAGTGCTGCTCACCTTCTTCTCAGCGTCG
 GCGGCTGCGACCAGCGGCCGAGGAAGGGGAGGAGAGAGGCCGATTGGC
 TGCGTACCACGTTTGATACTCAGTCACTTACCACAGCTGGTTCTCTTGTCG
 TTCAAATCTGGCTTGCCGCGCGCGCGCATTTTATTCTACCAGTTTGAATCT
 CCCACCTCTCCGACTGTAACGTCTCTAATTTGCTTCTCTCATCACTCTCTC
 TTTGCCATTCTCTCACTATCTAGACTCTATTTTTCCAGATGTCACCGCCGA
 CGAGACGGTACTCGCCACAACGACCAACACCACTTCCATGTCTGTGGAACC
 AACGGATCCGAGAAGCGCTGGTGAATCGTCTCAGATTCCGGAGCCAGACA
 CAATTGAGGTGAGGAAAAGTTTTGGGAATTTAAATCTGAATAAAACGTTTTCA
 GCAGCTGAAGGCAGAACAGCGCGAAGTGATGGCCGACGCGGCGAATGGTT
 CCGAAGTCAACGGAAATCAAGAGAACGGAAAAGAGGAAGCGGCATCTGCA
 GACGTGGAAGTGATCGAGATAGATGACACCGAAGAGTCTACGGATCCCTCA
 CCTGATGGATCTGATGAAAACGGTGATGCTGCATCTACATCGGTTCCAATC
 GAAGAGGAAGCGCGTAAAAAGGATGAGGGGGCTTCCGAAGTGACTGTGGC
 ATCATCTGAGATTGAACAAGACGATGATGGCGATGTTATGGAAATCACTGAG
 GAGCCGAACGGAAAGTCCGGAGGATACTGCCAACGGAACAGGTGTGTTTTAT
 AATTTTACCAAGTTTAATTTTAACTTTCTATTTTCAGTTACTGAGGAGGTGCTA
 GATGAAGAGGAGCCAGAACCTTCCGTAAACGGAACTGAGATCGCTACA
 GAGAAAGAGCCAGAAGATTCTTCAATGCCTGTGCAACAGAATGGGAAGGGT
 GTGAAGCGGCCTGTGCAATGCATCGAACTCGACGACGACGATGATGACGA
 GATTCAGGAAATTTCTACCCCTGCCCCAGCTAAAAAGCTAAAATTGATGAT
 GTCAAGGCGACAAGCGTTCCAGAAGAGGACAACAATGAGCAGGCGCAGAA
 GAGATTGCTCGACAAGCTGGAAGAGTATGTGAAGGAGCAGAAGGATCAACC
 ATCCAGCAAAAGCCGAAAAGTTCTGGACACTCTTCTCGGAGCAATCAATGC
 GCAAGTTCAAAGGAGCCTCTGTGCGTTCCGAAGCTGATCCTGGACAAAGT
 TCTCGTTCTCCCAAACACAATATCATTTCCACCAAGTCAAGTTTGCGACTTAT
 TGATTGAGCAGATCCCGAAATGCCTTTGACGAAGGTTATCAACAGGATGTT
 TGGAGAAGAAAGACCAAAGTTGAGTGATTCCGAGAAACGAGAGAGAGCTCA
 GCTGAAACAACATAATCCTGTTCCAAATATGACAAAACCTGCTCGTGGACATT
 GGACAGGATCTCGTTCAAGAAGCTACCTATTGTGATATAGTTTACGCGGAAGA
 ATCTTCCAGAGGTGCCAAAAAATCTTGAAACCTATAAGCAAGTCGCTGCGCA
 GTTGAAACCAGTTTGGGAGACATTGAAACGCAAAATGAGGCGTACAAGTT
 GAAAATGCATCGATGCGACGTCTGTGGATTCCAGACGGAATCAAAGCTGGT
 TATGAGCACTCACAAGGAGAATTTGCACTTCACAGGATCCAAATTCCAGTGC
 ACCATGTGTAAAGAGACGGACACGAGTGAGCAAAGAATGAAGGATCACTAC
 TTGTAAGTTTTTTTTTTTTCATCTTTCAATATTCATTTAATTACAGCGAAACTC
 ATCTTGTTATTGCAAAATCGGAAGAGAAGGAGTCCAAGTATCCATGTGCAAT

FIGURE 2

CTGCGAAGAAGACTTCAATTTCAAAGGTGTCGGTGAGCAGCATTACAAGCA
GTGCAAGAAGGACTACATTCGCATTCGAAACATCATGATGCCGAAGCAAGA
CGATCATCTCTATATCAACAGATGGCTCTGGGAGAGGCCCAATTGGATCC
CAGCATTCTTCAACAGCAGCAACAAGCTGCTCTTCAGCAAGCTCAACAAAAG
AAGCAACAGCAACTTCTGCATCAACAGCAAGCAGCACAAGCTGCAGCCGCT
GCGCAACTCTTACGGAAGCAACAATTACAACAGCAACAACAACAGCAACAG
GCTCGTCTTCGTGAGCAACAGCAAGCGGCCCAATTCCGGCAAGTGGCTCAA
CTGCTGCAACAACAATCAGCGCAGGCTCAACGTGCACAGCAGAATCAAGGA
AATGTGAATCATAACACTCTGATTGCAGGTAATAGCTAAACATATTTTAAATA
AGTATTTTGTATAATTATTTATATTTTCAGCAATGCAAGCGTCGTTGCGTAGAG
GTGGTCAACAAGGAAATTCGCTGGCAGTTTCTCAACTTCTCCAAAAGCAAAT
GGCAGCTTTGAAGTCGCAACAAGGAGCTCAACAACCTTCAGGCTGCGGTGAA
CTCCATGAGAAGCCAGAACAGTCAAAAGACGCCAACACACAGAAGTTCGAA
ACTTGTTACTACGCCGTCTCATGCTACTGTTGGCTCTTCTTCAGCTCCCACG
TTTGTATGCGAAATTTGTGATGCGTCAGTGCAGGAAAAGGAGAAGTATCTAC
AGCATCTTCAGGTAATTTTAAGAAACGTTTCTATTTCAATTTCAAACCGATT
ATTAATATCTTAACATCACATTTTCAGACTACTCATAAGCAGATGGTTGGA
AAAGTGCTGCAGGACATGTCGCAAGGAGCTCCACTGGCATGTTCTCGATGC
CGTGACAGATTCTGGACTTATGAAGGGTTGGAGCGGCACTTGGTGATGTCG
CATGGTCTCGTCACTGCTGATCTGCTCCTCAAAGCGCAAAGAAGGAAGAC
GGAGGTGATGCAAGACATGCGGCAAGAACTATGCGTTCAACATGCTTCAA
CACTTGGTAGCTGATCATCAAGTGAAGTTGTGCTCGGCTGAAATCATGTACT
CGTGCGATGTGTGCGCGTTCAAATGCTCGAGTTATCAGACTCTGGAAGCCC
ATCTCACTTCAAATCACCCAAAAGGAGATAAGAAGACATCAACACCAGCAAA
AAAAGATGATTGTATTACTCTGGATGATTAAATAGGAAAACGAATGGCTTATC
CCGTTCTACGAATGAGTGCTGGAAACATTCTTCACAATGATCTCAATTATTC
TCTTATTCTTTACATTCAATCATTTTAAATCACCAAGTTCTCCCACTTTCATTGA
TATACACATTCTATTGCGGGTTCCGGAACCGAAATCAATCAGTACTTTACTTT
ATTTCCCAATTTTTCTCTTCATGATATCTGGTTTATTCTCGCATCTTCCCCTA
CCTTCAAACTCCCTATTTTTTTTTTCAAACCTAACTACCCCAACAATTATCATG
TAAATCAAATTGCAATCCCCATAAGACAGATCAGTATACACTTTCACTTCA
TACGTCTGTTGTTCTCCCCATCTCATACTTTTTTACCATTGTCCAGTTAA
GATTTTGAAGATATCTAT

FIGURE 3

mep-1 ORF

ATGGTCACCGCCGACGAGACGGTACTCGCCACAACGACCAACACCACTTCC
 ATGTCTGTGGAACCAACGGATCCGAGAAGCGCTGGTGAATCGTCCTCAGAT
 TCGGAGCCAGACACAATTGAGCAGCTGAAGGCAGAACAGCGCGAAGTGAT
 GGCCGACGCGGCGAATGGTTCCGAAGTCAACGGAAATCAAGAGAACGGAA
 AAGAGGAAGCGGCATCTGCAGACGTGGAAGTGATCGAGATAGATGACACC
 GAAGAGTCTACGGATCCCTCACCTGATGGATCTGATGAAAACGGTGATGCT
 GCATCTACATCGGTTCCAATCGAAGAGGAAGCGCGTAAAAAGGATGAGGGG
 GCTTCCGAAGTGAATGTGGCATCATCTGAGATTGAACAAGACGATGATGGC
 GATGTTATGGAAATCACTGAGGAGCCGAACGGAAAGTCGGAGGATACTGCC
 AACGGAACAGTTACTGAGGAGGTGCTAGATGAAGAGGAGCCAGAACCCTTCC
 GTAAACGGAACAACCTGAGATCGCTACAGAGAAAGAGCCAGAAGATTCTTCA
 ATGCCTGTCGAACAGAATGGGAAGGGTGTGAAGCGGCCTGTCGAATGCAT
 CGAACTCGACGACGACGATGATGACGAGATTCAGGAAATTTCTACCCCTGC
 CCCAGCTAAAAAAGCTAAAATTGATGATGTCAAGGCGACAAGCGTTCCAGA
 AGAGGACAACAATGAGCAGGCGCAGAAGAGATTGCTCGACAAGCTGGAAG
 AGTATGTGAAGGAGCAGAAGGATCAACCATCCAGCAAAAGCCGAAAAGTTC
 TGGACACTCTTCTCGGAGCAATCAATGCGCAAGTTCAAAGGAGCCTCTGT
 CGGTTCGGAAGCTGATCCTGGACAAAGTTCTCGTTCTCCCAAACACAATATC
 ATTCCCACCAAGTCAAGTTTGCGACTTATTGATTGAGCACGATCCCGAAATG
 CCTTTGACGAAGGTTATCAACAGGATGTTTGGAGAAGAAAGACCAAAGTTGA
 GTGATTCCGAGAAACGAGAGAGAGCTCAGCTGAAACAACATAATCCTGTTCC
 CAAATATGACAAAACCTGCTCGTGGACATTGGACAGGATCTCGTTCAAGAAG
 CTACCTATTGTGATATAGTTCACGCGAAGAATCTTCCAGAGGTGCCAAAAAA
 TCTTGAAACCTATAAGCAAGTCGCTGCGCAGTTGAAACCAGTTTGGGAGAC
 ATTGAAACGCAAAAATGAGCCGTACAAGTTGAAAATGCATCGATGCGACGT
 CTGTGGATTCCAGACGGAATCAAAGCTGGTTATGAGCACTCACAAGGAGAA
 TTTGCACTTCACAGGATCCAAATTCAGTGCACCATGTGTAAAGAGACGGAC
 ACGAGTGAGCAAAGAATGAAGGATCACTACTTCGAAACTCATCTTGTTATTG
 CAAAATCGGAAGAGAAGGAGTCCAAGTATCCATGTGCAATCTGCGAAGAAG
 ACTTCAATTTCAAAGGTGTCCGTGAGCAGCATTACAAGCAGTGCAAGAAGG
 ACTACATTCGCATTGAAACATCATGATGCCGAAGCAAGACGATCATCTCTA
 TATCAACAGATGGCTCTGGGAGAGGCCCAATTGGATCCAGCATTCTTCA
 ACAGCAGCAACAAGCTGCTCTTCAGCAAGCTCAACAAAAGAAGCAACAGCA
 ACTTCTGCATCAACAGCAAGCAGCACAAGCTGCAGCCGCTGCGCAACTCTT
 ACGGAAGCAACAATTACAACAGCAACAACAACAGCAACAGGCTCGTCTTCG
 TGAGCAACAGCAAGCGGCCCAATTCCGGCAAGTGGCTCAACTGCTGCAACA
 ACAATCAGCGCAGGCTCAACGTGCACAGCAGAATCAAGGAAATGTGAATCA
 TAACACTCTGATTGCAGCAATGCAAGCGTCGTTGCGTAGAGGTGGTCAACA
 AGGAAATTCGCTGGCAGTTTCTCAACTTCTCCAAAAGCAAATGGCAGCTTTG
 AAGTCGCAACAAGGAGCTCAACAACCTTCAGGCTGCGGTGAACTCCATGAGA
 AGCCAGAACAGTCAAAGACGCCAACACACAGAACTCCCACGTTTGTATGC
 GAAATTTGTGATGCGTCAGTGCAGGAAAAGGAGAAGTATCTACAGCATCTTC
 AGACTACTCATAAGCAGATGGTTGGAAAAGTGCTGCAGGACATGTCGCAAG
 GAGCTCCACTGGCATGTTCTCGATGCCGTGACAGATTCTGGACTTATGAAG
 GGTTGGAGCGGCACTTGGTGATGTGCGCATGGTCTCGTCACTGCTGATCTGC

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FIGURE 3

TCCTCAAAGCGCAAAAGAAGGAAGACGGAGGTCGATGCAAGACATGCGGC
AAGAACTATGCGTTCAACATGCTTCAACACTTGGTAGCTGATCATCAAGTGA
AGTTGTGCTCGGCTGAAATCATGTACTCGTGCGATGTGTGCGCGTTCAAAT
GCTCGAGTTATCAGACTCTGGAAGCCCATCTCACTTCAAATCACCCAAAAGG
AGATAAGAAGACATCAACACCAGCAAAAAAAGATGATTGTATTACTCTGGAT
GATTAA

FIGURE 4

MEP-1 protein

MVTADETVLATTNTTSMVSVEPTDPRSAGESSSDSEPTDIEQLKAEQREVMAD
AANGSEVNGNQENGKEEAASADVEVIEIDDEESTDPSPDGSDENGDAASTSV
PIEEEARKKDEGASEVTVASSEIEQDDDGDMVEITEEPNGKSEDTANGTVTEEV
LDEEEPEPSVNGTTEIATEKEPEDSSMPVEQNGKGVKRPVECIELDDDDDDDEIQ
EISTPAPAKKAKIDDKATSVPEEDNNEQAQKRLDKLEEYVKEQKQDPSSKSR
KVLDTLLGAINAQVQKEPLSVRKLILDKVLVLPNTISFPPSQVCDLLIEHDPEMPL
TKVINRMFGEERPKLSDSEKRERAQLKQHNPPVPMNTKLLVDIGQDLVQEATYC
DIVHAKNLPEVPKNLETYKQVAAQLKPVWETLKRKNPYKLMHRCDVCGFQT
ESKLVMSHKNLHFTGSKFQCTMCKETDTSEGRMKDHYFETHLVIKSEEKE
SKYPCAICEEDFNFKGVREQHYKQCKKDYIRIRNIMMPKQDDHLYINRWLWER
PQLDPSILQQQQQAALQQAQKKQQQLLHQQQAAQAAAAAQLLRKQQLQQQ
QQQQQARLREQQQAAQFRQVAQLLQQQSAQAQRAQQNQGNVNHNTLIAAM
QASLRRGGQGGNSLAVSOLLQKQMAALKSQQGAQQLQAAVNSMRSONSQKT
PTHRTPTFVCEICDASVQEKELYLQHLQTTHKQMVGKVLQDMSQGAPLACSR
CRDRFWTYEGLERHLVMSHGLVTADLLLKAQKKEDGGRCKTCGKNYAFNMLQ
HLVADHQVKLCSAEIMYSCDVCAFKCSSYQTLAHLTSNHPKGDKKTSTPAKK
DDCITLDD

FIGURE 5

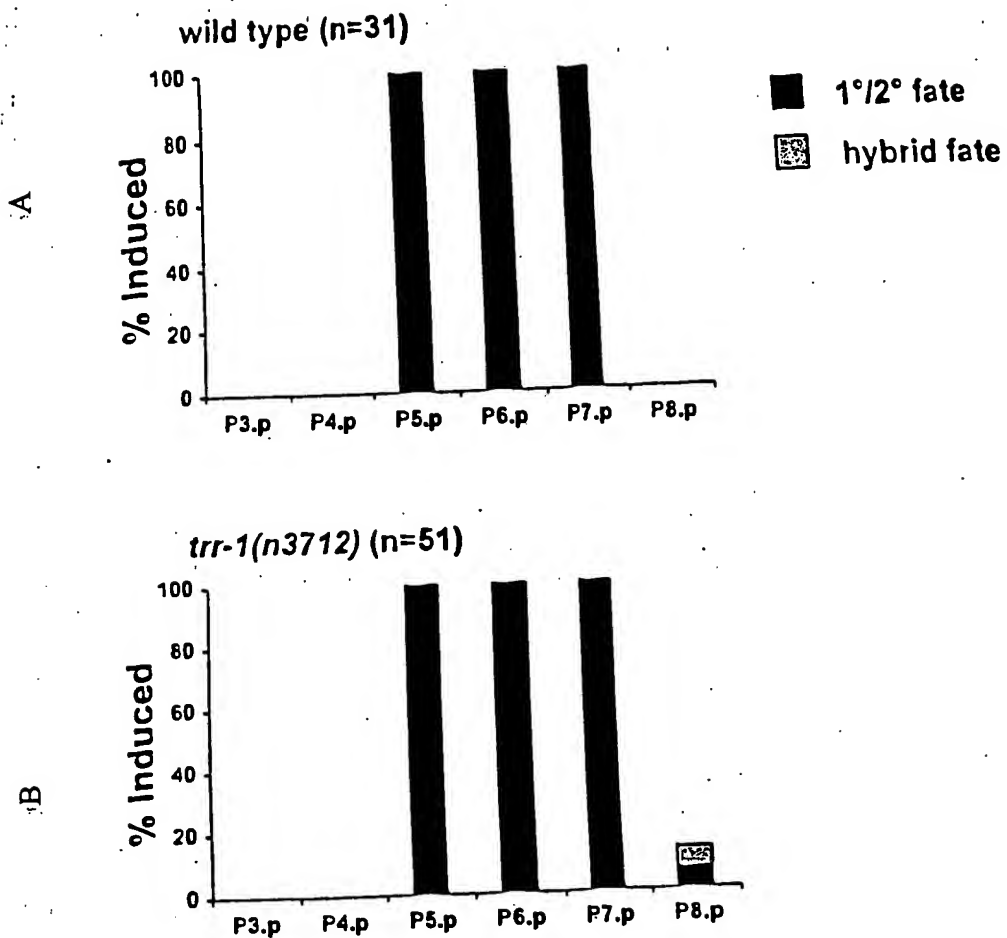
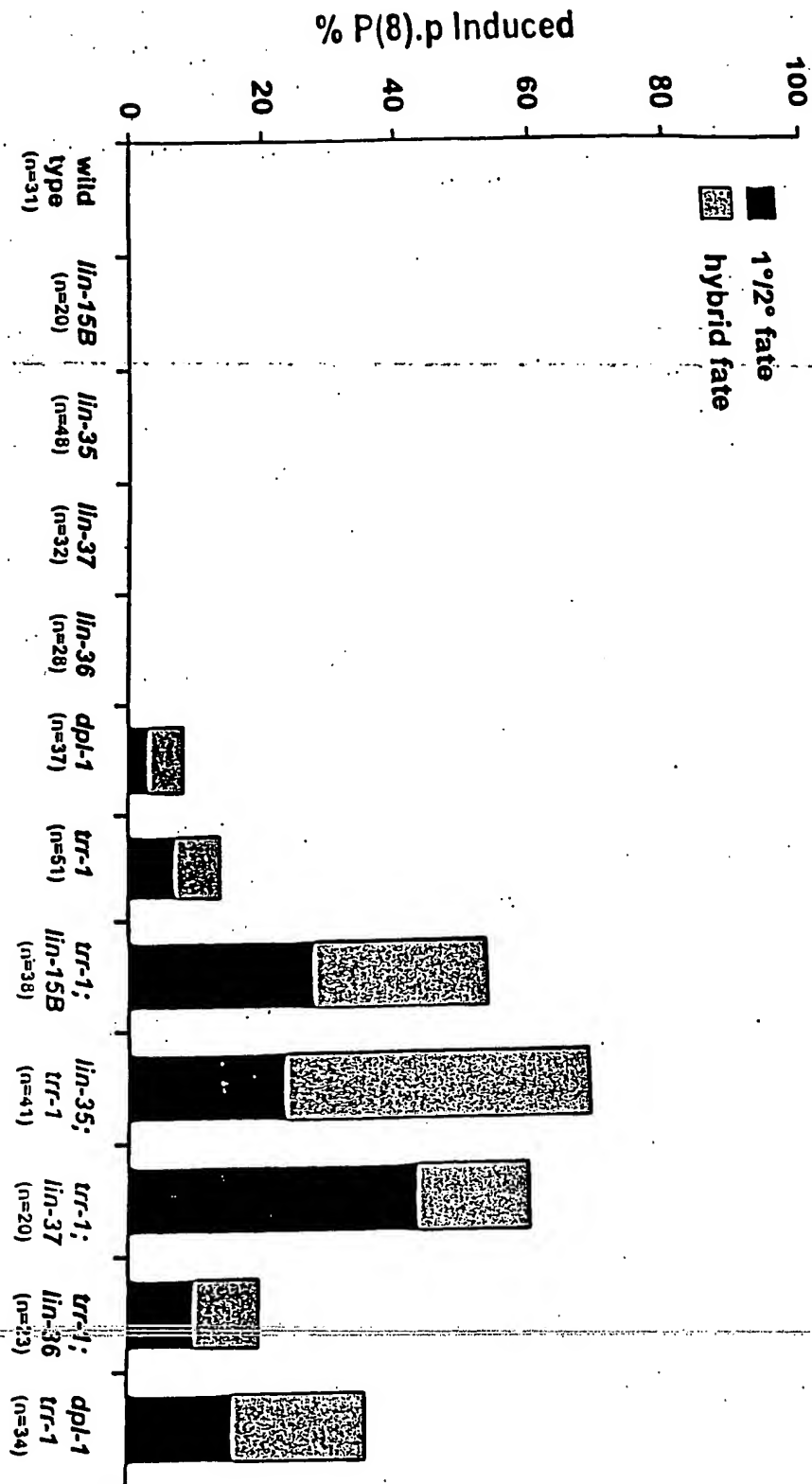


FIGURE 6



Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING

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FIGURE 7

A.



B.

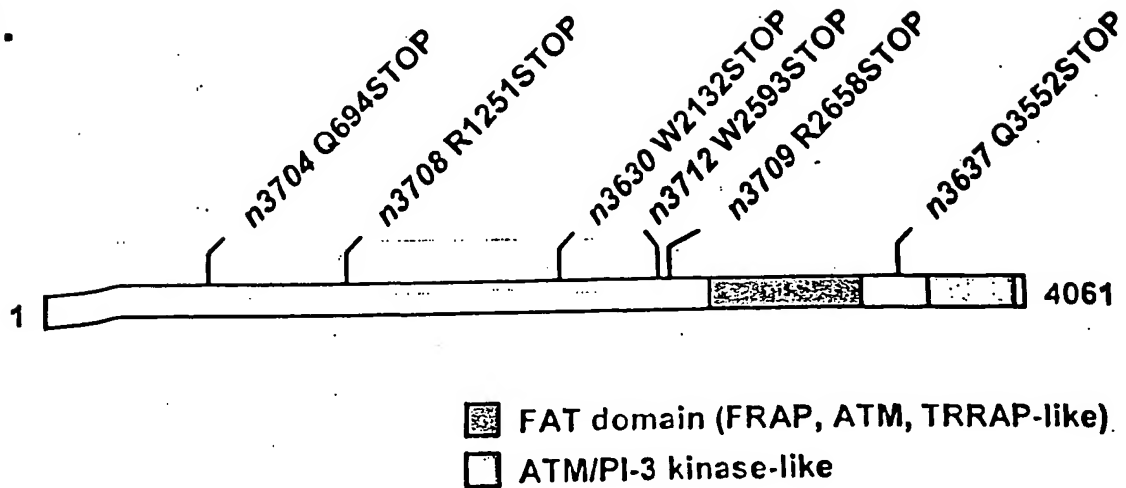


FIGURE 8

trr-1 genomic sequence:

GAGGAA GATGTAGACGACGATTCCGGTTCCGTA CTCTCATGACTTTTGGCG
 AAAATCCTCACGAATCTTTTTCCGTCATACGTTGAGTTAAAAATCTGGCGAT
 GTAACGAAGAATGAGAAGAGCGTTTGATGTTTGCCATAAGTAGATTTTACTG
 AAATAAGAAAAAGCTTTAATTAAATATAATGATGATTTTTTTTTTCCAACCTCACT
 TTTCCGATTGTTCTGATGTTTTAGTTCTGTGGCTCTGCGAAGGAAAAGTCG
 AATAAATGCAGCGAAATTTCTGTTGTTTGTGTATTGTACATTAGACATTGAA
 GATGATCATCTAAAGCAGATCCAAAGCGATTCCGGTGTCTCTAAACGATTA
 TAACATTTTTAAAGCTTTTGCCATAATTTAATCCTTACTCGTCGTCATCATCAA
 ACTTGAGACTGAAAGAGAGAAGTTTGTTCCAAAATGGGTCATAATCGTCGAC
 AGGTTCCAAACCGCTGAGTTTCTTCAGATAAATATTCTCCTGTAAGACCGTT
 TCCTTGTTATAACTGATCCCATGTGTCTGAAATTTGTTATTACACTGTTAAT
 AATCATAAAAATAAAAAGAAAAAGTCAAGAAAGGGTCAAATATTAATCAGGTCA
 CATCTTTTTTATTCAATAAAATCTCCTCTCTCGTTTCGTGGCAATGCACGTGAA
 ATGCGCCAACAACCGCGAGTGCGCCAACACACACACATACGCGTCAGCAG
 ACAATTCGCTCTCGTTTGAAATTTAGTTGTTTCTTTGTTTCTGCTGAAATAAT
 GTCAGTTTTCCGATAATTTAGCGTTTCTGACTGATTTTTCTTGTTGCATTCT
 ACTTCCTAATAGTTCATTCTACTCCATTCTTCATTTTATAATCTGTTTCCTTCG
 CAATTTAGTGAATTAACACGTAAATCTTGTTTCAGATAAATTATTCAAATAGT
 TGCACAAAGCTCAATAGTTTAGAAGTATCTTCAGTGCTGGTCACTAATACAA
 AATCGATCCGGCTATGGCTTCTCCAGGCTATCGGTCTGTGCAGTCCGATCG
 GAGTAATCACCTAACAGAGCTGGAAACGAGAATTCAAATCTTGCCGATAAT
 TCACAAAGAGATGATGTCAAATTGAAAATGTTACAAGTTAGTTTCAATAATTC
 GTGTTAAGTAATCAATTTGTTCCGGTTGCAGGAGATTTGGAGCACAATCGAAA
 ATCATTTCACACTAAGTTCGCACGAGAAAGTCGTGGAGAGGCTCATTCTCTC
 GTTCCTACAAGTTTTCTGCAACACAAGTCCACAGTTCATTGCTGAAAACAAT
 ACACAACAGCTTCGAAAGTTAATGCTTGAAATCATTCTTCGACTTTTGAACG
 TAGAAGCCATGAAACATCATAGCAAAGAAATTATCAAGCAGATGATGAGGCT
 AATCACCGTGGAAAATGAGGAGAATGCCAATTTGGCTATCAAATTTGTCACC
 GATCAAGGGAGAAGTACCGGCAAATGCAATATTGCGGAGAGGTTTTCACAG
 ATAATGGTCTCCTTCAAACAATGGTCATTGATCTGACGGCGAGTGGTCTGA
 GCTGGTGATATGTTCAACATAAAAGAGCATAAAGCTCCACCGTCAACTAGCT
 CCGACGAGCAAGTCATCACTGAATATTTGAAGACTTGCTACTATCAACAAAC
 GGTTCTTCTCAACGGAACGGAAGGAAAACCGCCATTAAAATACAATATGATT
 CCATCAGCTCATCAGTCAACGAAGGTGCTCCTGGAGGTTCCGTATCTCGTG
 ATTTTCTTCTATCAACATTTCAAACAGCGATCCAAACCGAAGCGCTTGATT
 CATGAGGCTTGGTCTTGATTTTCTAAATGTCAGAGTTCCAGACGAGGATAAA
 CTCAAAACAATCAAATAATAACCGATGATTTTGTGAGTGCACAGTCCCGAT
 TCCTGTCAATTCGTCAACATTATGGCTAAGATTCCAGCGGTAAAGTTTCGTTTTT
 TCAAGTTTTTTTTCTGTAATCCIGATTTTTATTTTTAGTTTATGGATCTTATCA
 TGCAAAATGGACCGCTTCTAGTGTCGGGAACAATGCAGATGCTCGAGCGGT
 GCCCGGTGATCTGATAAGTGTCGACGAGAAGTTCTGATGGCTTTGAAGT
 ATTTACATCTGGAGAAATGAAGTCGAAATCTTTCCAATGCTACCTCGACT
 CATCGCTGAGGAGGTTGTTCTGGGAACAGGATTCACTGCGATTGAGCATTT
 GCGAGTTTTCATGTATCAAATGCTAGCAGATCTGTTGCATCACATGCGAAAT
 TCTATAGACTATGAAATGATCACACAGTAAGTTTGAATAAGACTTTCTGATGA

FIGURE 8

AAAATGTTGAAATTTACGCGTGATTTTCGTATTCTGTGCGCACTCTTCACGATC
 CTAACAACTCTTCTCAAGTCCAGATTATGTCTGCTCGGCTGCTCAACTCACT
 GGCCGAATCTCTGTGCAAATGGATTCACATGATACCGTAAGACTTATTCTA
 TCAATAATCGTATCTCACTTCGAAATAAGTTTCAGACTCGTGATCTGCTCATT
 GAAATCCTGGAGTCGCACGTGGCCAAGCTCAAACTCTTGCAGTCTATCAG
 ATGCCTATTCTCTTCCAACAATACGGAACCGAAATAGACTACGAATACAAAA
 GTTATGAGAGAGACGCCGAGAAACCTGGAATGAATATCCCAAAGGACACTA
 TACGAGGAGTACCGAAACGAAGAATCCGTGCGGCTCTCCATTGATTCAGTTG
 AAGAGCTGGAATTCCTGGCATCAGAACCATCCACGTGCGGAAGATGCAGATG
 AGAGTGGTGGAGATCCGAACAAGCTTCTCCGCCAACAAAAGAGGGGAAAGA
 AAACGTCTCCCGAAGCGATTTTAACCGCCATGTCAACGATGACACCTCCTC
 CATTGGCAATTGTTGAAGCTCGAAATCTTGTGAAGTATATAATGCATACGTG
 TAAATTCTGTGACAGGACAATTGAGAATCGCCCGGCCATCACAGGATATGTAT
 CATTGTTGGAAGGAGCGAGATTTATTGAAACGTCTTCTACGATATGGTGTA
 TGTGTATGGATGTATTCTGTGCTTCCAACAACCTCGAAATCAACCACAAATGCA
 TTCTTCAATGCGGACAAAAGATGAGAAAGATGCTCTGGAGTCGTTGGCAA
 CGTTTTTACAACAATCGACCATGCGATATTCCGGGAAATCTTCGAAAAGTAT
 ATGGATTTCTTGATTGAAAGAATTTACAATCGGAACTATCCATTGCAATTGAT
 GGTGAACACCTTCTTGGTTCGAAATGAAGTGCCATTCTTTCGCATCTACGATG
 CTTTCATTCTTGATGTCTCGAATGAAATTGCTGGAAGTTAGCAATGACAAGA
 CGATGCTATATGTGAAGCTCTTCAAATTATCTTCTCCGCCATCGGAGCCAA
 TGGCTCTGGGCTTCATGGAGATAAAATGCTCACTTCATACCTCCCAGAGATT
 CTCAAACAGTCAACTGTCTTGGCATTAAACAGCTCGTGAACCTCTCAACTATT
 TCCTTTTGCTTCGTGCATTGTTCCGCGAGTATTGGTGGTGGCGCTCAGGATAT
 TTTGTATGGAAAGTTCCTGCAGTTACTGCCAAATCTTCTTCAATTCTTGAATA
 AATTGACGGTGAGTTTCATTTTTTGATATATCGGTAATACACTAAAAATCCAG
 AATCTTCAGTCATGTCAACATCGGATTCAAATGCGTGAGCTCTTCGTGAGT
 TGTGTTTGACTGTGCCAGTTCGACTCAGTTCCTTCTGCCATACCTACCGCT
 TCTGATGGATCCACTGGTGTGTGCGATGAATGGGAGTCCGAACATAGTTAC
 ACAAGGATTGAGAACATTGGAATTATGTGTGGATAACTTGCAACCTGAATAT
 CTTCTCGAAAATATGCTTCCTGTCCGTGGAGCTTTGATGCAAGGCCTCTGG
 CGTGTGTTGATCGAAAGCTCCAGATACATCATCGATGACAGCAGCGTTCAGG
 ATCCTCGGAAAGTTCGGAGGAGCCAATCGAAAACCTTCTGAATCAACCGCAA
 ATTCTTCAAGTAGCCACTTTAGGCGACGTAAGTTTATTTAGTTTATTCTCTTC
 CTCGTTTTAAGTTCTAACATTGATCCTATTAACAGACTGTTGAGTCGTACATC
 AATATGGAATTCTCGCGGATGGGACTCGATGGCAATCACAGCATTACCTG
 CCACTGTCCGAGTTGATGAGAGTCGTTGCCGATCAGATGAGATATCCAGCT
 GATATGATCCTTAATCCAAGTCCTGCAATGATCCCGTCAACTCATATGAAGA
 AATGGTGTATGGAATTGTGCAAAGCCGTCTTGTTAGCCGGACTTGATCTTC
 AGGAAGCCCAATTACTCCAAGTGCAAATCTTCCGAAGATTATCAAGAACTT
 CTTGAAGATTTTGATCCAAACAATCGTACCACTGAAGTATACACATGTCCGA
 GGGAAAGTGATCGAGAGCTTTTTGTGAATGCACTTCTCGCAATGGCTTGTA
 GTTCTTAAGTTCTTTTCTCTAATCAGATCTATATTTTAAATTTTTCAGACGG
 AATATGGAATAAAGACGGTTTCCGGCATGTCTATAGCAAATTCCTTATCAAA
 GTTCTCCGCCAGTTTGC GTTGATTGGAGTACTCGAATACATTGGTGGAAATG
 GATGGATGCGTCATGCAGAAGAGGAAGGTGTTCTACCATTGTGCCTTGACT

FIGURE 8

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CGTCTGTTATGGTTGATGCTCTGATTATTTGTCTCTCTGAAACATCGTCAAG
CTTCATCATTGCTGGTGTCTCTCTCGTCATATCAATGAGACTCTCTCG
CTTACACTTCCCGATATTGATCAAATGTCGAAAGTTCCAATGTGCAAATAGT
GATGGAGAAGGTGTTCAAATTGTGTACGGGCCTGCTTGGTATGCAAGATC
TGGTGGAAATCAATGCAATTGGATACATGATCGAATCGTTTCCACGAAAATTT
GTTATGGACTTTGTGATAGATGTTGTTGATTGATCATGGAAGTTATTTTGG
GAACTGTTGAAGAAATATCAAGTGGATCTGCTGATTCTGCATACGATTGTCT
CAAGAAAATGATGCGAGTCTATTTTATCAAAGAAGAAGGCCAAGAAGAGGA
GAATCTGACACTCGCGACTATTTTTGTGTCTGCAATCTCTAAGCATTACTTCC
ACAGTAATGAAAGAGTCAAGAGAATTTGCGATTGGTTTAATGGATCATTGTAT
GGTTCACTCAAGACTTGCACCATCCCTTGATAAGTTCTACTATCGATTCAAG
GAGTTCTTTGAGCCAGAATTAATGCGGGTGCTCACAACAGTTCCAACAATGT
CATTGGCAGACGCAGGAGGAAGTTTGGATGGAGTTCAAACTATATGTTCA
ACTGTCCGGATGGTTTTGATTTGAAAAAGATATGGACATGTACAAGCGATA
TTTGTCACATCTGCTGGATATTGCACAAACCGATACATTTACCTTAAACCAA
GGAATGCCTTCAAAAAATGCGAGACATGCCCATCGCATTTCCTTCCCTCATT
CCCAATCACTACACATATTGATTCAATGCGAGCCAGTGCTCTACAGTGTCTT
GTGATCGCGTATGATCGAATGAAGAAGCAATACATCGACAAGGGAATAGAG
CTGGGTGATGAGCATAAGATGATAGAGATCCTCGCACTTCGCAGCTCCAAG
ATCACAGTTGATCAAGTCTACGAGAGCGATGAATCTTGGAGACGATTGATGA
CAGTTCTATTGAGAGCAGTCACTGACAGAGAACTCCTGAAATTGCGGAGA
AGCTTCATCCTTCACTTTTGAAGGTCTCACCAATATCCACAATCATCATCGCA
ACATTTGGTGCTTCTTACATAAGAAATATTAGTGGAGCAGGAGATGACAGTG
ATTCAGATCGTCATATTTCTGACAACGATATAATGAAGTTCAAGTGTCTCGTG
GAGCTCAATCCAAAGATTCTGGTCACAAAAATGGCAGTGAATCTCGCAAATC
AAATGGTTAAATATAAGATGAGTGACAAGATCTCTAGGATTTTGTGAGTTCC
CAGTAGCTTCACTGAAGAGGAGCTCGATGATTTGGAAGCGGAGAGATGAA
AGGAATTCGAGAGTTGGATATGATTGGTCATACGGTTAAATGCTTGCTGGA
TGCCCAAGTGACCACATTCACGGAGCAAATTATTGTGGATATCAGTCGTTTTG
CTGCTCATTTTGAGTATGCTTATTCGCAAGATGTACTTGTAATTGGATTGAT
GATGTCACAGTAATCCTCAACAAAAGTCCCAAAGATGTATGGAAGTTCTTCT
TGTCTCGAGAATCAATTCTAGATCCTGCACGCAGATCCTTTATTGGAAGAAT
CATAGTCTATCAATCAAGTGGTCCACTGCGACAGGAATTCATGGATACTCCG
GAATATTTTGAGAACTCATTGATCTTGACGATGAGGAGAATAAGGATGAAG
ATGAGAGAAAAATCTGGGATCGTGATATGTTTGCATTTTCGATTGTGATCG
TATCTCGAAGAGCTGCCCTGAGTGGCTTATTTCTCCGAATTCCTCAATTCCA
AGAATTAAGAAGTTGTTCTCCGAAACGGAATTCATGAGCGATATGTGGTTC
GAGCATTGACTGAGGTGAAGAAATTTCAAGAAGAGATCATAGTGAAACGGA
TGACAGAGCACAAGTACAAGGTTCCGAAGCTGATTCTGAATACCTTCTGA
GATATTTGAGGTAATTTCAAGATAGTTTGTAAAAATTAATTACAAAGAAATATA
CCAAACTGAACCCCAAAAAAATTTTGAATTTTCGGATCAAAAAAATTTAA
TATTTTCTCGAAAAATCCTTCAAAATACCAAAAAATTCGAATTCTCACTTCTAA
AATTATTTTGAATTTTAAATAATTTTGAACATTTCTCTATGAAATTCATGTT
TTGGGCCTATTTCAAGGCTATAAAAAATTTTCTGATTTTAAATAACTTGCAA
ATTTCAAGGCTCAACATCTATGACTACGATCTATTCATCGTTATCGCCTCGTGT
TTCAATGGCAATTTCTGTCACCGATCTCTCTTTTCTTCGCGAATATCTTGAAC

FIGURE 8

TGAAGTCATCCCGAAAGTGCCGTTACAATGGCGGAGAGAGCTGTTTCTTCG
AATTATGCAGAAGTTTGATACGGATCCACAACTGCTGGAACAAGTATGCAG
CATGTGAAGGCCCTTCAATATTTGGTTATTCCCACGTTGCATTGGGCGTTG
AGCGATATGATACGGATGAAATTGTTGGCACCGCACCAATAGATGATTGCG
ATTCTTCGATGGATGTAGATCCGGCAGGCAGCTCGGATAACCTTGTGGCTC
GTTTAACATCAGTCATTGATTCTCATCGTAATTATCTGAGCGATGGAATGGT
CATTGTTTTCTATCAACTTTGCACATTGTTCTACAAAACGCCTCCGAACATA
TTCACAATAATAACTGCAAGAAACAAGGTGGACGCCTACGGATCCTGATGCT
CTTCGCCCTGGCCGTGCCTGACCATGTACAATCATCAAGATCCAACAATGCG
GTACACTGGATTCTTCTTCTTGGCCAATATTATAGAGCGTTTACAATTAATC
GGAAAATCGTGCTTCAAGTGTTCCATCAACTTATGACTACTTATCAGCAGGA
CACTAGAGATCAAATCCGGAAAGCCATTGATATATTAAGTCCAGCTTTGAGG
ACACGAATGGAAGATGGACACTTGCAAATATTGAGTCATGTGAAGAAAATTC
TTATCGAAGAATGCCATAATTTGCAACATGTTGAGCATGTTTTGTAAGTTTAT
TATCTAAAATGATTTTTTTTAAATGTTAAAAATTTAATTTTAAAATGCGTTCGTG
CTCCTTTAATAATTCTGAATTTTCCAGCCAAATGGTGGTTCGCAATTATCGT
GTCTACTATCATGTTGATTGGAGCTTCTCACGCCTCTTCTGAACGGAGTTC
AACGAGCACTTGTGATGCCAAATAGTGTTCTGGAAAAGTAAGTTTCCAGCCC
GTTGTTGTAAGTCACTCCCTTGTAAATATTTAGCTGGCAAAGTTCGACGTCA
TGCGGTGGAGATCTGCGAGATGGTCATCAAGTGGGAATTGTTGAGAAGCT
GAAAACAGATCATATTATCAGTGACGAAGAAGCTCTCGAAGTTGACAAGCAA
TTGGATAAGCTGCGAACAGCTTCATCCACAGATCGTTTCGATTTCGAGGAG
GCTCATAACAAGAGAGACATGCCTGATGCTCAACGCACGATTATCAAAGAG
CACGCCGATGTGATTGTCAATATGCTTGTCCGATTCTGTATGACGTTCCATC
AGAATTCGGGTTCTTCGTCCACTTCTCAAAGTGGGAACCATGGTGTGAGTT
GACCAAAAAATGTGAGCTGCTTCTACGTGCAGCCCTACGACCAAGCATGTG
GGGAGAATTTGTGAGCTTCCGATTAACAATGATCGAAAAGTTTTTGTCAATT
CCGAATGATAATGCTCTACGCAATGATATAAGTTCTACGGCCTACGCTAATA
CTATCCAAAATGCACAACACACTCTGGATATGCTGTGTAATATTATTCCTGTT
ATGCCAAAAGTAGCTTGTGACTATGATGAGACAAGTCCAACGGCCACTCA
TACAATGTCTCAATAACGGAGCTCAGGTATGTGAAGAAGCATGAATAGGGG
GTTATAAATCACTAATTTCTCTTAGAACTTTAAGATGACTCGTCTTGTCACTC
AAATTGTCAGTCGGTTACTCGAAAAGACAAATGTTTCGGTTAACGGGCTTGA
TGAGCTGGAGCAATTGAATCAATACATTTCCCGATTCTTACATGAACATTTT
GGATCTCTTTTGAAGTAAGTTTTATTTTTGAATTTCCATCTTTCAACCCTTCGC
CAGTTGCAGAACTTGAGTGGACCAGTGTTGGGAGTTCTCGGAGCATTTC
TCTTTTGCGAACAATTTGTGGACACGAGCCAGCATACTTGGATCATTTGATG
CCTTCATTTGTAAAAGTGATGGAGAGAGCTGCAAAAAGAGCACTTGGCGTAT
GTTGCCAACTCGCAAGATGGAAATATGGTGAAGAGTAAGTTCTATAAAAAGA
TTCAGATTTTCTAATCCCCTTAGATTCTTTCCAGATGTTGCTGAATTGTTGT
GTGCATGCATGGAGCTGGTACGTCCCAGAGTCGATCATATCAGTATGGAGA
TTAAGAGATCAATTGTTGGTGGTATTATCGCGGAGCTGATTATCAAATCGAA
TCACGATAAGATCATCCAGACGTGAGTGAAGCTTCTCGGAGCAATGATTAG
CACGCAGGATATGGAATTTACAATTCTCACTGTTCTTCCGCTACTTGTTGCT
ATCCAATCAATTATTGTGACCAAGTTCAAGAATTGCAAGGATCTGATAGCAG
ACTATCTTGTGTGGTTATTACCGTTTTTGGAGAACAGCGAATATCGGAACTC

FIGURE 8

GGAAGCTGGATCTCGTCTCTGGGAAGGATTCTTCTGGGGACTCAAGAGTAG
CGATCCTCAAACCCGGGAGAAATTCTCGATAGTTTGGGAGAAGACTTGGCC
ACACATGGCAACAGTAGATATTGCTCATCGAATGAAATATATCATGCAAAAT
CAAGATTGGTCCAAGTTCAAACACGCGTTTTGGTTGAAATTCGCACTTTGGG
GAATGCTACGAACGATTGCCAAACGGCCAACTGATCCGAATAATAAGAGAA
AGAAAGTGATACTGTTGAACTGTGCAACTCCATGGAGAACAATTGAATATGC
AGCGAAATTGAAGGATCAGCCAATGGAAGTGGAACTGAAATGAAACGAGA
AGAGCCAGAACCGATGGAAGTTGACGAAAAAGACTCGCAAGATGATTCTAA
GGATGCCGGGAGAGCCCAAGGAGAAGGAAAAGCTCACATTGGAATTATTGCT
TGCTGGACAACAAGAACTTTTGGATGAAGCTTCCAATTATGATTTTGCGGAT
GCTCTAGATACAGTATCCCAGATTACATTTGCACTTAATGGTAAATTGTTCAA
AGTTTATGAATATTTTTCTTAAAAATCACAATTTTCAGAGAATCAAGTGACAA
GCAAGATGTGGGTTAGTGTTGTTCAAATCATTCTGGAGTTCCTTATCACAATC
CGAAATCGAAGATTTTACGGCGCTAGTCGTTCCGTTTATGAGCAGTGGAGT
GCATAATAATTATCAGACGGGTGTACAGGATAGTGTGCTTGCTGTTTGGCTT
GAAGCTGTTGGTGACGCTGTTTCAATTTGCCGTCCAGATTGATTGAGGTACGTT
CTGAAAATGAATGCTGGAAAAAATTCGATTTTTCTGTTTAAAAAAAGTTAAAA
TTTCCGATTTTTTGAATAGCAAAAAAAGAAAAACATTTATTTTGAAAAAAGA
GTCCTCACCGGAATTTTTTAATAAATAAATTTAAAAAAGAAAAAAACTAAA
AACTTCAATTTTTGAAAATCAAAAAAATTAACAGAAACAGACGAGGTAAAA
AATTTTAAAAAAGTTCTGTAAAAAATGGAGAATCACAGTTTTCGTTGTCTT
TTCTGAAAAAATTTGAAAAATTAATAATTAAACGATTTTTTGGTTTTAATTTA
AAAAATATACGAAAAAAGACTGAAGAATTTTTTGTCAAAAAAATTTGATT
TTGATGAGGGAAAAAGTTCAAAAACTTGGAGAAATCATCGGAAATTTTAGAA
GATTCAATAAAAAATTTCCAAAAAATAATTGAACATTTATGATTTTTGGGTAT
TTTGAATAATTGAAAAATTACGCTTAATTTTTAGATTAAAAAATCAAAAAA
ACCAACACTCCTTTTGAACTTGACACTTTTGAAACGTTTTTTTTTTTGAAT
AATAAATTTCTCATTTTCAATTTATCTCATCAAAACACGAATGCTGGCATAACG
GAATCAGGCTTCTCGAGAATCATATATGGACAATCCAAAGCAACTCAACAA
CACGTTACTCCGAGAAATGAAAGTGGCACCAGGTCTCGCTGGAGATATTGA
GACACTCGAATCTCTTGGAACTCTACAATGAGATATCAGAGTTTGATCAG
TTCTGCTGCAATCTGGGAACGCCGTGCTGTATTTCTGATACGATGAGAGCA
ATGTCAGCTATGCAATTGGGAGATATGGAATTAGCTCAATCTTATCTGGAAA
AATCAATGAGCAGTACGTATGAACTCTTGCTCCGACAATCAATCGTAAGTT
TGGATCAATCGGTTGTACTTCTCACACAAAATAGTATTCCTTTGAGCAAAACAA
CACTTCAAATTCGGAGAAGCATGTTTCTCCGATTATTGACAAAGAATACGAT
CATTGGATGGAGATGTACATCACAAATTGCTCGGAGCTTCTTCAGTGGCAAA
ATGTGGCCGACGTATGCAATGGCAAAGACATGCAACATGTTCTGGCCTGA
TCAACGCAGCATCTCACATTCGGGACTGGAATGTGGTTCGAGGAGTGTAATA
GTCAGATAGCTGGATGTATCCACCAAGTTTCCATTTAGATTACACTCTTTTC
AATTTGATGAGTACTGTTATGGTTAGTTTAAAGTCAAAAAGTGATATATAATTA
TTGTTTAAATTTTTCAGCGAATGAATGAAAACCTCAAGCCCGACACATATGAAG
GAACGATGCAAAATTGCAATTCAAGAGTGCACAGAAGCTCATATTAGTCGTT
GGAGAGCACTTCCGTCAGTTGTTTCATATGGTCATGTCAAGATTCTTCAGGC
AATGAACTTGGTTCGAGAAATTGAAGAGTCTACAGATATTGCGATTGCTCTG
CTCGAGGCCCATCAAACAAAGTGGATCAGGCGTTGATGGGCGATATGAAG

FIGURE 8

TCGTTGATGAAAGTATTCCGAAATAGAACACCAACCACTTCGGATGATATGG
GATTCGTTTCGACTTGGTATGATTGGAGGAATCAGATTCATGGAATGATGCT
TCAAAGATTCTGAATATTGGGATAAAGTAGGACTCAACGTCGCTGCAACTGGA
AACCAGTCAATTGTTCCGATTCAATGGCTCAAGCACAGTTGGCCGTAG
CCAAACATGCCAAGAATCTTGATTCCATAATTTAACGAAAGATCTACTCAA
CAAATTAGCTGGATTGACAGCCATACCGATGATGGATGCTCAAGATAAAGTT
TGCACTTACGGCAAGACACTTCGCGATATGGCAAACAGTGCGGCTGACGAA
AGAGTGAAAAATGAGCTATTGTGTGAAGCGCTTGAAGTTTTGGAAGATGTGC
GAATTGATGATCTACAGAAGGATCAGGTTGCTGCATTGCTTTATCATCGTGC
TAATATTCATTCAGTTCTTGATCAGTAAGTTTTCAATGCCGAAAAAAATTA
AGTTTTACAAAAATAAATTTAGAGCTGAAAATGCTGACTACACCTTCTCCGC
AGCCTCTCAACTTGTGACTTGCAAATAGTGTGACAACCACTGGAATCAAG
CTCATGAAAAATTGGGGCCACCATCTTTACAAGAGATTCTTCTCTACGACAG
TTTGCAAGGAAACCGGAAACAACTTCGGACGGCAGGCTCTCGCTTGTTACT
TCATTGCGGCTCGTGTGGATAACGATATCAAGGCGAGAAAACCGATTGCCA
AGATTTTGTGGCTCTCGAAGCACTTGAATGCGTGTGGATCACATGAAGTGAT
GAATCGGGTTATTAAGAAGCAACTTCATTCACTTAATCTCTTCAATTGGCTTT
ACTGGCTTCCACAATTGGTTACTGATGTTGATATAAAACCAAATTCGAACCTT
GTTCTGATTCTCTGCAAGGTAAGTTTTGAAATATTTAAATATTTTCAGAATTTT
AAATGAAATTCATTTGCAGATGGCTGCTGCTCATCCACTTCAAGTATTTACC
ACATTCGGGAGGCAGTTAGCGTTGACGATATTGACTCGGTTCTCGAAGAAG
ATTACACTGATGAGCAAATGTCGATGGATGTTTCGGATGAGGATTGTTTTGC
AGACGATCCACCATTTGATAGAATTCTGAAAATATGTCTGAAATATCGTCCAA
CTGATATTCGAGTCTTCCATCGTGTCTCTCAAAGAACTTGACGAGATGAATGA
GACATGGGTGAACGTCCTTGCGTCATGCGATCTGCCTCAAGGATCAGAT
GTTCAAAGATTTCTCGGAACAAATGGACGCGACGTTCAATGAGATGCAATAT
TCGGAGGATGTGACTATGATGACGTTGAGATGGAGGAAACAGCTGGAAGAA
GACTTGGTGTATTTCCAACAGAATTATAATCTTGATTTCCTGGAGATTCGTAA
CAAGCGAAAGATGATCGTGACGAAGGGATGTATGGGAGTCGAGAAAAGTCA
GATAATGTTGAAAAAGAGCTGAGTCAAGTGTTACAGAGCCGGCCGGCAT
GCAAGATGAATTTGATTTTGTACAAATATGACTAATATGATGGTCTCACAGT
TGGATATTCATGCAGTCGATGCTCCACGCCCTCAGGGATATATTGCTATTGT
TCTCGACTGGATTGAGCGATTTCGTGCTGTTTCGATCGACTTCCACGAAG
AATCCCTCTGGAATCGTCAAGCCCATATCTCGCCAGATTCAGCCATCGTACA
GGATGCATCGAAATGCCATACGATTTGCTCAACGTTTTGCGCGCCAAGAAT
CATACTCTGATGGCTTCCAATCAAACGGGGCAATACATATCCATGCTCTCTC
GATTTGAGCCAACTTTGAGATTGTGATCAAAGGTGGTCAAGTGATAAGAAA
GATCTATATTCGAGGACAAACCGGAAAGAGTGCGGGCGTTTTATCTGAAGAA
ATCTGTGCAGGATGAGCCAATAACCGAGTTCCACAAATGTTCAAACATCTT
GATCACGTTCTACAAACCGATAGAGAGTCGGCGGAGAAGACATCTTCATGCT
CCAACAGTGCTGCAGATGAGAGTCGGACAGAAGACGACACTCTACGAAGTT
GCATCCGTTCAACCATATGCAATGCCACCGGATTGTACCAGAACTATCCAG
CATACAAATCGACATTGTTTCATCCATATGATGTGCTGACTGCCACTTTCAAT
GGAAGTTATTATCCGGATGATATGGTATTGCACTTCTTTGAGAGATTGCCCC
AAAGTTCTTCATCCATCGGACAACCTCTTCCAACCTCCGACGAACCAAGATGG
AACAGTTGCTCCGCCACGACTAACGGAAGCTCACCACATCAAGAATATTATT

FIGURE 8

TATGAGTACGTTTGAGAAGCTAGTGTCTAAAATAATAATTAATGTAAAAAAT
 TTTTCAGAGACTTTGCCCCGAGATATGATCCCATTCGACTTCTCTACGACTAC
 CTCACCTGCACGATATCCTGATCCGGTTATGTACTATGCAATGAAGAAGCAAT
 TGCTGCACAGTCTCGCCGTCTATCCACAATCGAATATCATTGCAATCTGAC
 ACCAATGGGACCTGATCAAATGATGATGACAATGAATACTGGAGTCCTTAGC
 AATCCTTCATATAGATTGAAATCCGAGGAGGACGATCACTTCATGATATTC
 AACACTTTGGACATGAAGTTCATTCCGATTGACTCCAAATCTATCGATTTTG
 GTTGGTGTTCACAGGATGGTGACTTGTATGGAGTATGGCTGCTGCGTCA
 AAATGTTTGATGAAGAAGGAACCTGAAGTTATCATGAGACCGTTAGTATGGG
 ATGAATTCGCCAACAATACAGATTGCGACAAATCGGTAATTTTACTTTAATAT
 GCTAATAGGGAATTGAACTAATGTTTTCCAAGCGTTTGCAGGTATTCGCGTG
 TCATGCATCGAATTCTTACATCAATGGTGTGCGGAGCAAGCTTCGAAACACG
 AATAGCGCCGACGCCAACTCAGAAAGGACGATTGTGTGTGCTGATCAGT
 CGAGCCAAGGATTCCGATAATCTGGCCCGAATGCCACCCACCTACCACGC
 GTGGTTCAGATCTCATAATTACCGTTCTCTATTTTGATCCCGCCTCCCACTC
 TCACAGATCTCTATACATTTGTCAAATGTTTCCAATCTTTTATCTGCCATA
 CATTTCGTTTTATTGTTTTGTTTCTTTCTTTCTTTATTTCTTTCTAACTTTA
 AGATTTATGTAAATATTTAACTGCGCTGGTATTTATGAAAAATTCAGATAAAG
 TTTTCAAGTTTAAAAAATCGAAAATTCGAAGTCGGAAGTTCTCTTACAGGTGT
 AGTAAGTAGGCACAATGGCAATAGGTACATGGAAGGCTTGCGGAAGGCACA
 TGGGTAGGCATAAGATCGAAAAATAAGCTGATATATAAATATAGATAGGTAT
 TGGTTAGGCACAAATTAGGCACGTAGGTGTGAGCTGGCAAATAGGTAGGCA
 TGACGTTTCGGCAAATCGGCAAATTGCCGATTGGCGAAAATTTTCAAATCCG
 GCGATTGCGCGGAAATGTTTAGAGAAATTTTTATAAGACAGAAAACTTACA
 ACTGTGTCTTTTGAATTTCTTCCGGTTTTCTTTATACAGTGCGTGCAACTTC
 TATAGCGCCCCCCCCCCCCCCCCCCCCCTATTTTTTCGCGTTTCACGCC
 ATTCTGATTTTTATTTTTCTGATTTTTTTTTTTTTGCACTGAAACTTGGCATTGA
 GGATGCTTGGAGAGAAATATCAGCCAGCAAAATAAAGAATCTGGTCAACTCA
 ATGTCGAATAGATTTTTGAGGTTATCGTTAAGAAGGGAGGTCCCACGACGT
 ATTGATCCTTCATCGAGTTAACAAATTATGATGTTTTAATTGATTTCAATCCAC
 TTCTGGACACAGAAGGACGAATAGTGCAATCTGGTACAAGTTTATCACCACC
 TACAACTTCGTGATTTGTGGAAAATCTTTCAGACATGTCTCCATGAGTGTC
 TCAGAACATCTTGGTCAGGTTTGGAGTCGATCCACCGCTGGGAGCCGAGA
 ATGGGCCTCTAACAC

FIGURE 9

lrr-1 ORF sequence

ATGGATCCGGCTATGGCTTCTCCAGGCTATCGGTCTGTGCAGTCCGATCGG
 AGTAATCACCTAACAGAGCTGGAACGAGAATTCAAATCTTGCCGATAATT
 CACAAAGAGATGATGTCAAATTGAAAATGTTACAAGAGATTTGGAGCACAAT
 CGAAAATCATTTCACTAAGTTTCGCACGAGAAAGTCGTGGAGAGGCTCATT
 CTCTCGTTCCTACAAGTTTTCTGCAACACAAGTCCACAGTTCATTGCTGAAA
 ACAATACACAACAGCTTCGAAAGTTAATGCTTGAAATCATTCTTCGACTTTG
 AACGTAGAAGCCATGAAACATCATAGCAAAGAAATTATCAAGCAGATGATGA
 GGCTAATCACCGTGGAAAATGAGGAGAATGCCAATTTGGCTATCAAATTTGT
 CACCGATCAAGGGGAGAAGTACCGGCAAATGCAATATTGCGGAGAGGTTTC
 ACAGATAATGGTCTCCTTCAAACAATGGTCATTGATCTGACGGCGAGTGGT
 CGAGCTGGTGATATGTTCAACATAAAAGAGCATAAAGCTCCACCGTCAACTA
 GCTCCGACGAGCAAGTCATCACTGAATATTTGAAGACTTGCTACTATCAACA
 AACGGTTCCTTCTCAACGGAACGGAAGGAAAACCGCCATTAATAACAATATG
 ATTCCATCAGCTCATCAGTCAACGAAGGTGCTCCTGGAGGTTCCGTATCTC
 GTGATTTTCTTCTATCAACATTTCAAACAGCGATCCAAACCGAAGCGCTTG
 ATTTGATGAGGCTTGGTCTTGATTTTCTAATGTCAGAGTTCCAGACGAGGA
 TAAACTCAAACAAATCAAATAATAACCGATGATTTTGTGAGTGCACAGTCCC
 GATTCCTGTCAATCGTCAACATTATGGCTAAGATTCCAGCGTTTATGGATCTT
 ATCATGCAAATGGACCGCTTCTAGTGTCCGGAACAATGCAGATGCTCGAG
 CGGTGCCCGGCTGATCTGATAAGTGTCCGACGAGAAGTTCTGATGGCTTTG
 AAGTATTTACATCTGGAGAAATGAAGTCGAAATCTTTCCAATGCTACCTC
 GACTCATCGCTGAGGAGGTTGTTCTGGGAACAGGATTCACTGCGATTGAGC
 ATTTGCGAGTTTTCATGTATCAAATGCTAGCAGATCTGTTGCATCACATGCG
 AAATTCTATAGACTATGAAATGATCACACACGTGATTTTCTGATTCTGTGCGA
 CTCTTCACGATCCTAACAACCTCTTCTCAAGTCCAGATTATGTCTGCTCGGCT
 GCTCAACTCACTGGCCGAATCTCTGTGCAAATGGATTCACATGATACCTTT
 CAGACTCGTGATCTGCTCATTGAAATCCTGGAGTCGCACGTGGCCAAGCTC
 AAACTCTTGCAGTCTATCACATGCCTATTCTCTTCCAACAATACGGAACCG
 AAATAGACTACGAATACAAAAGTTATGAGAGAGACGCCGAGAAACCTGGAA
 TGAATATCCCAAAGGACACTATACGAGGAGTACCGAAACGAAGAATCCGTC
 GGCTCTCCATTGATTCAGTTGAAGAGCTGGAATTCCTGGCATCAGAACCATC
 CACGTCGGAAGATGCAGATGAGAGTGGTGGAGATCCGAACAAGCTTCCTCC
 GCCAACAAAAGAGGGGAAAGAAAACGTCTCCCGAAGCGATTTTAACCGCCAT
 GTC AACGATGACACCTCCTCCATTGGCAATTGTTGAAGCTCGAAATCTTG
 AAGTATATAATGCATACGTGTAAATTCGTGACAGGACAATTGAGAATCGCCC
 GGCCATCACAGGATATGTATCATTGTTGGAAGGAGCGAGATTTATTGGAACG
 TCTTCTACGATATGGTGTAAATGTGTATGGATGTATTGCTGCTTCCAACAAC
 CGAAATCAACCACAAATGCATTCTTCAATGCGGACAAAAGATGAGAAAGATG
 CTCTGGAGTCGTTGGCAAACGTTTTACAACAATCGACCATGCGATATTCCG
 GGAAATCTTCGAAAAGTATATGGATTTCTTGATTGAAAGAATTTACAATCGGA
 ACTATCCATTGCAATTGATGGTGAACACCTTCTTGGTTGGAATGAAGTGCC
 ATTCTTCGCATCTACGATGCTTTTATTCTTGATGTCTCGAATGAAATTGCTGG
 AAGTTAGCAATGACAAGACGATGCTATATGTGAAGCTCTTCAAATTTATCTTC
 TCCGCCATCGGAGCCAATGGCTCTGGGCTTCATGGAGATAAAATGCTCACT
 TCATACCTCCCAGAGATTCTCAAACAGTCAACTGTCTTGGCATTAAACAGCTC

FIGURE 9

GTGAACCTCTCAACTATTTCTTTTGCTTCGTGCATTGTTCCGCAGTATTGGT
GGTGGCGCTCAGGATAATTTGTATGGAAAGTTCCTGCAGTTACTGCCAAATC
TTCTTCAATCTTGAATAAATTGACGAATCTTCAGTCATGTCAACATCGGATT
CAAAATGCGTGAGCTCTTCGTGAGTTGTGTTTGAAGTGTGCCAGTTGACTCA
GTTCCCTTCTGCCATACCTACCGCTTCTGATGGATCCACTGGTGTGTGCGAT
GAATGGGAGTCCGAACATAGTTACACAAGGATTGAGAACATTGGAATTATGT
GTGGATAACTTGCAACCTGAATATCTTCTCGAAAATATGCTTCCTGTCCGTG
GAGCTTTGATGCAAGGCCTCTGGCGTGTGATCGAAAGCTCCAGATACAT
CATCGATGACAGCAGCGTTGAGGATCCTCGGAAAGTTCGGAGGAGCCAATC
GAAAACCTTCTGAATCAACCGCAAATTCTTCAAGTAGCCACTTTAGGCGACAC
TGTTTCAGTCGTACATCAATATGGAATTCTCGCGGATGGGACTCGATGGCAAT
CACAGCATTACCTGCCACTGTCCGAGTTGATGAGAGTCGTTGCCGATCAG
ATGAGATATCCAGCTGATATGATCCTTAATCCAAGTCTGCAATGATCCCGT
CAACTCATATGAAGAAATGGTGTATGGAATTGTGAAAGCCGTCTTGTTAGC
CGGACTTGGATCTTCAGGAAGCCCAATTACTCCAAGTGCAAATCTCCGAA
GATTATCAAGAACTTCTTGAAGATTTTGTATCCAAACAATCGTACCACTGAAG
TATACACATGTCCGAGGGAAAGTGATCGAGAGCTTTTGTGAATGCACTTCT
CGCAATGGCTTACGGAATATGGAATAAGACGGTTTCCGGCATGTCTATAG
CAAATTCTTTATCAAAGTTCTCCGCCAGTTTGCCTTGATTGGAGTACTCGAA
TACATTGGTGGAAATGGATGGATGCGTCATGCAGAAGAGGAAGGTGTTCTA
CCATTGTGCCTTGACTCGTCTGTTATGGTTGATGCTCTGATTATTTGTCTCTC
TGAAACATCGTCAAGCTTCATCATTGCTGGTGTCTCTCTTCGTCATATC
AATGAGACTCTCTCGCTTACACTTCCCGATATTGATCAAATGTGAAAGTTC
CAATGTGCAAATACTTGATGGAGAAGGTGTTCAAATTGTGTACGGGCCTG
CTTGGTATGCAAGATCTGGTGGAAATCAATGCAATTGGATACATGATCGAATC
GTTTCCACGAAAATTTGTTATGGACTTTGTGATAGATGTTGTTGATTGATCA
TGGAAGTTATTTTGGGAAGTGTGAAAGAAATATCAAGTGGATCTGCTGATTC
TGCATACGATTGTCTCAAGAAATGATGCGAGTCTATTTTCATCAAAGAAGAA
GGCCAAGAAGAGGAGAATCTGACACTCGCGACTATTTTGTGTCTGCAATCT
CTAAGCATTACTTCCACAGTAATGAAAGAGTCAGAGAATTTGCGATTGGTTT
AATGGATCATTGTATGGTTCACTCAAGACTTGCACCATCCCTTGATAAGTTC
TACTATCGATTCAAGGAGTTCTTTGAGCCAGAATTAATGCGGGTGCTCACAA
CAGTTCCAACAATGTCATTGGCAGACGCAGGAGGAAGTTTGGATGGAGTTC
AAAACATATGTTCAACTGTCCGGATGGTTTTGATTTGAAAAAGATATGGA
CATGTACAAGCGATATTTGTACATCTGCTGGATATTGCACAAACCGATACA
TTTACCTTAAACCAAAGGAATGCCTTCAAAAAATGCGAGACATGCCCATCGC
ATTTCTTCTCCTCCATTCCCAATCACTACACATATTGATTCAATGCGAGCCAGT
GCTCTACAGTGTCTTGTGATCGCGTATGATCGAATGAAGAAGCAATACATCG
ACAAGGGAATAGAGCTGGGTGATGAGCATAAGATGATAGAGATCCTCGCAC
TTCGCAGCTCCAAGATCACAGTTGATCAAGTCTACGAGAGCGATGAATCTTG
GAGACGATTGATGACAGTTCTATTGAGAGCAGTCACTGACAGAGAACTCC
TGAAATTGCGGAGAAGCTTCATCCTTCACTTTTGAAGGTCTCACCAATATCC
ACAATCATCATCGCAACATTTGGTGCTTCTTACATAAGAAATATTAGTGGAG
CAGGAGATGACAGTGATTGAGATCGTCATATTTCTGACAAACGATATAATGAA
GTTCAAGTGTCTCGTGGAGCTCAATCCAAAGATTCTGGTCACAAAAATGGCA
GTGAATCTCGCAAATCAAATGGTTAAATATAAGATGAGTGACAAGATCTCTA

FIGURE 9

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE LET-60 RAS SIGNALING
Applicant(s): Horvitz et al.
Filing Date: September 12, 2003 Serial No.: N/A
Page 19 of 91 Customer No.: 21559

GGATTTTGT CAGTTCCCAGTAGCTTCACTGAAGAGGAGCTCGATGATTT CGA
AGCGGAGAAGATGAAAGGAATTCGAGAGTTGGATATGATTGGTCATACGGT
TAAAATGCTTGCTGGATGCCAGTGACCACATTCACGGAGCAAATTATTGTG
GATATCAGTCGTTTTGCTGCTCATTTTGAGTATGCTTATTCGCAAGATGTACT
TGTA AATTGGATTGATGATGTCACAGTAATCCTCAACAAAAGTCCCAAAGAT
GTATGGAAGTTCTTCTGTCTCGAGAATCAATTCTAGATCCTGCACGCAGAT
CCTTTATTCGAAGAATCATAGTCTATCAATCAAGTGGTCCACTGCGACAGGA
ATTCATGGATACTCCGGAATATTTTGAGAACTCATTGATCTTGACGATGAG
GAGAATAAGGATGAAGATGAGAGAAAAATCTGGGATCGTGATATGTTTGCAT
TTTCGATTGTGCGATCGTATCTCGAAGAGCTGCCCTGAGTGGCTTATTTCTCC
GAATTCCCCAATTCCAAGAATTAAGAAGTTGTTCTCCGAAACGGAATTCAAT
GAGCGATATGTGGTTCGAGCATTGACTGAGGTGAAGAAATTTCAAGAAGAG
ATCATAGTGAAACGGATGACAGAGCACAAGTACAAGGTTCCGAAGCTGATT
CTGAATACCTTCCTGAGATATTTGAGGCTCAACATCTATGACTACGATCTATT
CATCGTTATCGCCTCGTGTTTCAATGGCAATTTCTGTCACCGATCTCTCTTTTC
TTCGCGAATATCTTGAAACTGAAGTCATCCCGAAAGTGCCGTTACAATGGCG
GAGAGAGCTGTTTCTTGAATTATGCAGAAGTTTGATACGGATCCACAACT
GCTGGAACAAGTATGCAGCATGTGAAGGCCCTTCAATATTTGGTTATTCCCA
CGTTGCATTGGGCGTTTCGAGCGATATGATACGGATGAAATTGTTGGCACCG
CACCAATAGATGATTCCGATTCTTCGATGGATGTAGATCCGGCAGGCAGCT
CGGATAACCTTGTGGCTCGTTTAACATCAGTCATTGATTCTCATCGTAATTAT
CTGAGCGATGGAATGGTCATTGTTTTCTATCAACTTTGCACATTGTTCTGATC
AAAACGCCTCCGAACATATTCACAATAATAACTGCAAGAAACAAGGTGGACG
CCTACGGATCCTGATGCTCTTCGCCTGGCCGTGCCTGACCATGTACAATCA
TCAAGATCCAACAATGCGGTACACTGGATTCTTCTTCTTGGCCAATATTATA
GAGCGTTTCACAATTAATCGGAAAATCGTGCTTCAAGTGTTCCATCAACTTA
TGACTACTTATCAGCAGGACACTAGAGATCAAATCCGGAAAGCCATTGATAT
ATTA ACTCCAGCTTTGAGGACACGAATGGAAGATGGACACTTGCAAATATTG
AGTCATGTGAAGAAAATTTCTATCGAAGAATGCCATAATTTGCAACATGTTCA
GCATGTTTTCCAAATGGTGGTTTCGAATTATCGTGTCTACTATCATGTTTCGAT
TGGAGCTTCTCACGCCTCTTCTGAACGGAGTTCAACGAGCACTTGTGATGC
CAAATAGTGTTCTGGAAAATTTAGCTGGCAAACCTCGACGTCATGCGGTGG
AGATCTGCGAGATGGTCATCAAGTGGGAATTGTTCAGAACGCTGAAAACAG
ATCATATTATCAGTGACGAAGAAGCTCTCGAAGTTGACAAGCAATTGGATAA
GCTGCGAACAGCTTCATCCACAGATCGTTTCGATTTCGAGGAGGCTCATAA
CAAGAGAGACATGCCTGATGCTCAACGCACGATTATCAAAGAGCACGCCGA
TGTGATTGTCAATATGCTTGTCCGATTCTGTATGACGTTCCATCAGAATTG
GGTCTTTCGTCCACTTCTCAAAGTGGGAACCATGGTGTGAGTTGACCAA
AAATGTCAGCTGCTTCTACGTGCAGCCCTACGACCAAGCATGTGGGGAGAA
TTTGT CAGCTTCCGATTAACAATGATCGAAAAGTTTTTGTC AATTCCGAATGA
TAATGCTCTACGCAATGATATAAGTTCTACGGCCTACGCTAATACTATCCAA
AATGCACAACACACTCTGGATATGCTGTGTAATATTATTCCTGTTATGCCAAA
AACTAGCTTGATGACTATGATGAGACAACCTCCAACGGCCACTCATACAATGT
CTCAATAACGGAGCTCAGAACTTTAAGATGACTCGTCTTGTCACTCAAATTG
TCAGTCGGTTACTCGAAAAGACAAATGTTTCGGTTAACGGGCTTGATGAGCT
GGAGCAATTGAATCAATACATTTCCCGATTCTTACATGAACATTTTGGATCTC

FIGURE 9

TTTTGAATTGCAGAACTTGAGTGGACCAGTGTTGGGAGTTCTCGGAGCATT
TTCTCTTTTTCGAACAATTTGTGGACACGAGCCAGCATACTTGGATCATTG
ATGCCCTTCATTTGTAAAGTGATGGAGAGAGCTGCAAAAGAGCACTTGGCG
TATGTTGCGAACTCGCAAGATGGAAATATGGTGAAGAATTTCTTTCCAGATG
TTGCTGAATTGTTGTGTGCATGCATGGAGCTGGTACGTCCCAGAGTCGATC
ATATCAGTATGGAGATTAAGAGATCAATTGTTGGTGGTATTATCGCGGAGCT
GATTATCAAATCGAATCACGATAAGATCATCCAGACGTCAGTGAAGCTTCTC
GGAGCAATGATTAGCACGCAGGATATGGAATTTACAATTCTCACTGTTCTTC
CGCTACTTGTTTCGTATCCAATCAATTATTGTGACCAAGTTCAAGAATTGCAA
GGATCTGATAGCAGACTATCTTGTTGTGGTTATTACCGTTTTTGAGAACAGC
GAATATCGGAACTCGGAAGCTGGATCTCGTCTCTGGGAAGGATTCTTCTGG
GGACTCAAGAGTAGCGATCCTCAAACCCGGGAGAAATTCTCGATAGTTTGG
GAGAAGACTTGGCCACACATGGCAACAGTAGATATTGCTCATCGAATGAAAT
ATATCATGCAAAATCAAGATTGGTCCAAGTTCAAACACGCGTTTTGGTTGAA
ATTCGCACTTTGGGGAATGCTACGAACGATTGCCAAACGGCCAACCTGATCC
GAATAATAAGAGAAAGAAAGTGATACTGTTGAACTGTGCAACTCCATGGAGA
ACAATTGAATATGCAGCGAAATTGAAGGATCAGCCAATGGAAGTGGAACT
GAAATGAAACGAGAAGAGCCAGAACCGATGGAAGTTGACGAAAAAGACTCG
CAAGATGATTCTAAGGATGCCGGAGAGCCCAAGGAGAAGGAAAAGCTCACA
TTGGAATTATTGCTTGCTGGACAACAAGAACTTTTGATGAAGCTTCCAATT
ATGATTTTTCGGATGCTCTAGATACAGTATCCCAGATTACATTTGCACTTAAT
GAGAATCAAGTGACAAGCAAGATGTGGGTAGTGTTGTTCAAATCATTCTGGA
GTTCTTATCACAATCCGAAATCGAAGATTTACGGCGCTAGTCGTTCCGTT
TATGAGCAGTGGAGTGCATAATAATTATCAGACGGGTGTACAGGATAGTGT
GCTTGCTGTTTGGCTTGAAGCTGTTGGTGACGCTGTTCAATTTGCCGTCCAG
ATTGATTGAGTTTATCTCATCAAAACACGAATGCTGGCATACCGGAATCAGG
CTTCTCGAGAATCATATATGGACAATTCCAAAGCAACTCAACAACACGTTAC
TCCGAGAAATGAAAGTGGCACCAGGTCTCGCTGGAGATATTGAGACACTCG
AATCTCTTGGAACACTCTACAATGAGATATCAGAGTTTGATCAGTTTCGCTGC
AATCTGGGAACGCCGTGCTGTATTTCTGATACGATGAGAGCAATGTCAGC
TATGCAATTGGGAGATATGGAATTAGCTCAATCTTATCTGGAAAAATCAATG
AGCAGTACGTATGAACTCTTGCTCCGACAATCAATCCAAACAACACTTCAA
ATTCGGAGAAGCATGTTTCTCCGATTATTGACAAAGAATACGATCATTGGAT
GGAGATGTACATCACAAATTGCTCGGAGCTTCTTCAGTGGCAAAATGTGGC
CGACGTATGCAATGGCAAAGACATGCAACATGTTCTGGCCTGATCAACGC
AGCATCTCACATTCCGGACTGGAATGTGGTTCGAGGAGTGTAAGTTCAGAT
AGCTGGATGTATTCCACCAAGTTTCCATTTAGATTACACTCTTTTCAATTTGA
TGAGTACTGTTATGCGAATGAATGAAACTCAAGCCCGACACATATGAAGGA
ACGATGCAAAATTGCAATTCAAGAGTGCACAGAAGCTCATATTAGTCGTTGG
AGAGCACTTCCGTCAGTTGTTTCATATGGTCATGTCAAGATTCTTCAGGCAA
TGAACCTTGGTTCGAGAAATTGAAGAGTCTACAGATATTGCGATTGCTCTGCT
CGAGGCCCATCAAACAAAGTGGATCAGGCGTTGATGGGCGATATGAAGTC
GTTGATGAAAGTATTCCGAAATAGAACACCAACCACTTCGGATGATATGGGA
TTCGTTTCGACTTGGTATGATTGGAGGAATCAGATTCATGGAATGATGCTTC
AAAGATTGCAATATTGGGATAAAGTAGGACTCAACGTGCTGCAACTGGAAA
CCAGTCAATTGTTCCGATTCATTCAATGGCTCAAGCACAGTTGGCCGTAGCC

FIGURE 9

AAACATGCCAAGAATCTTGGATTCCATAATTTAACGAAAGATCTACTCAACAA
ATTAGCTGGATTGACAGCCATACCGATGATGGATGCTCAAGATAAAGTTTGC
ACTTACGGCAAGACACTTCGCGATATGGCAAACAGTGCGGCTGACGAAAGA
GTGAAAAATGAGCTATTGTGTGAAGCGCTTGAAGTTTGGGAAGATGTGCGAA
TTGATGATCTACAGAAGGATCAGGTTGCTGCATTGCTTTATCATCGTGCTAA
TATTCATTCACTTCTTGATCAAGCTGAAAATGCTGACTACACCTTCTCCGCA
GCCTCTCAACTTGTGCACTTGCAAAATAGTGTGACAACCACTGGAATCAAGC
TCATGAAAAATTGGGGCCACCATCTTTACAAGAGATTCTTCTCTACGACAGT
TTGCAAGGAAACCGGAAACAACCTTCGGACGGCAGGCTCTCGCTTGTTACTT
CATTGCGGCTCGTGTGGATAACGATATCAAGGCGAGAAAACCGATTGCCAA
GATTTTGTGGCTCTCGAAGCACTTGAATGCGTGTGGATCACATGAAGTGAT
GAATCGGGTTATTAAGAAGCAACTTCATTCACTTAATCTCTTCAATTGGCTTT
ACTGGCTTCCACAATTGGTTACTGATGTTGATATAAACCACAAATTCGAACCTT
GTTCTGATTCTCTGCAAGATGGCTGCTGCTCATCCACTTCAAGTATTTTACC
ACATTCGGGAGGCAGTTAGCGTTGACGATATTGACTCGGTTCTCGAAGAAG
ATTACACTGATGAGCAAATGTCGATGGATGTTTCGGATGAGGATTGTTTTGC
AGACGATCCACCATTGATAGAATTCTGAAAATATGTCTGAAATATCGTCCAA
CTGATATTGAGTCTTCCATCGTGTCTCAAAGAACTTGACGAGATGAATGA
GACATGGGTTGAACGTCACTTGCCTCATGCGATCTGCCTCAAGGATCAGAT
GTTCAAAGATTTCTCGGAACAAATGGACGCGACGTTCAATGAGATGCAATAT
TCGGAGGATGTGACTATGATGACGTTGAGATGGAGGAAACAGCTGGAAGAA
GACTTGGTGTATTTCCAACAGAATTATAATCTTGATTTCTTGAGATTCTGTA
CAAGCGAAAGATGATCGTGACGAAGGGATGTATGGGAGTCGAGAAAAGTCA
GATAATGTTGAAAAAGAGCTGAGTCAAGTGTTACAGAGCCGGCCGGCAT
GCAAGATGAATTTGATTTTGTCACAAATATGACTAATATGATGGTCTCACAGT
TGGATATTGATGACGTCGATGCTCCACGCCCTCAGGGATATATTGATTTGT
TCTCGACTGGATTGAGCGATTGCTGCTGCTTTCGATCGACTTCCACGAAG
AATCCCTCTGGAATCGTCAAGCCCATATCTCGCCAGATTGAGCCATCGTACA
GGATGCATCGAAATGCGATACGATTTGCTCAACGTTTTGCGCGCCAAGAAT
CATACTCTGATGGCTTCCAATCAAACGGGGCAATACATATCCATGCTCTCTC
GATTTGAGCCAAACTTTGAGATTGTGATCAAAGGTGGTCAAGTGATAAGAAA
GATCTATATTGAGGACAAACCGGAAAGAGTGCGGCGTTTTATCTGAAGAA
ATCTGTGCAGGATGAGCCAACTAACCAGATTCCACAAATGTTCAAACATCTT
GATCACGTTCTACAAACCGATAGAGAGTCGGCGAGAAGACATCTTCATGCT
CCAACAGTGCTGCAGATGAGAGTCGGACAGAAGACGACACTCTACGAAGTT
GCATCCGTTCAACCATATGCAATGCCACCGGATTGTACCAGAACTATCCAG
CATCACAAATCGACATTGTTTATCCATATGATGTGCTGACTGCCACTTTCAAT
GGAAGTTATTATCCGGATGATATGGTATTGCACTTCTTTGAGAGATTGCCCC
AAAGTTCTTCATCCATCGGACAACCTCTTCCAACCTCCGACGAACCAAGATGG
AAGAGTTGCTCCGCCACGACTAACGGAAGCTCACCACATCAAGAATATTATT
TATGAAGACTTTGCCCCGAGATATGATCCCATTCGACTTCTCTACGACTACC
TCACTGCACGATATCCTGATCCGGTTATGTACTATGCAATGAAGAAGCAATT
GCTGCACAGTCTCGCGGTGCTATCCACAATGGAATATCATTGCAATCTGACA
CCAATGGGACCTGATCAAATGATGATGACAATGAATACTGGAGTCCTTAGCA
ATCCTTCATATAGATTGCAAAATCCGAGGAGGACGATCACTTCATGATATTCA
ACACTTTGGACATGAAGTTCCATTCCGATTGACTCCAAATCTATCGATTTTG

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE LET-60 RAS SIGNALING
Applicant(s): Horvitz *et al.*
Filing Date: September 12, 2003 Serial No.: N/A
Page 21 of 91 Customer No.: 21559

FIGURE 9

GTTGGTGTTCACAGGATGGTGACTTGTTATGGAGTATGGCTGCTGCGTCA
AAATGTTTGATGAAGAAGGAACCTGAAGTTATCATGAGACCGTTAGTATGGG
ATGAATTCGCCAACAATACAGATTGCGACAAATCGCGTTTGCAGGTATTCGC
GTGTCATGCATCGAATTCTTACATCAATGGTGTGCGGAGCAAGCTTCGAAAC
ACGAATAGCGCCGACGCCAAACTCAGAAAGGACGATTGTGTGTGCTGATC
AGTCGAGCCAAGGATTCGGATAATCTGGCCCGAATGCCACCCACCTACCAC
GCGTGGTCTAG

FIGURE 10

TRR-1 protein sequence

MDPAMASPGYRSVQSDRSNHLTELETRIGNLADNSQRDDVKLKMLQEIWSTIE
 NHFTLSSHEKVVERLILSFLQVFCNTSPQFIAENNTQQLRKLMLEIILRLSNVEAM
 KHHSKEIHKQMMRLITVENEENANLAIKIVTDQGRSTGKMQYCGEVSQIMVSFKT
 MVIDLTASGRAGDMFNIKEHKAPPSTSSDEQVITEYLKTCYYQQTVLLNGTEGK
 PPLKYNMIPSAHQSTKVLLEVPYLVIFFYQHFKTAIQTEALDFMRLGLDFLNVRV
 PDEDKLKTNQIITDDFVSAQSRFLSFVNIMAKIPAFMDLIMQNGPLLVSQTMQML
 ERCPADLISVRREVLMAKYFTSGEMKSKFFPMLPRLIAEEVVLGTGFTAIEHLR
 VFMYQMLADLLHMRNSIDYEMITHVIFVFCRTLHDPNNSSQVQIMSARLLNSL
 AESLCKMDSHDTFQTRDLLIELESHVAKLKTAVYHMPILFQQYGTEIDYEYKSY
 ERDAEKPGMNIPKDTIRGVPKRRIRRLSIDSVEELEFLASEPSTSEDADESGGDP
 NKLPPPTKEGKTSPEAILTAMSTMTPPPLAIVEARNLVKYIMHTCKFVTGQLRIA
 RPSQDMYHCSKERDLFERLLRYGVMCMDFVLPTRNQPMHSSMRTKDEK
 DAESLANVFTTIDHAIFREIFEKYMDFLIERIYNRNYPLQLMVNTFLVRNEVPFF
 ASTMLSFLMSRMKLLEVSNDKTMLYVKLFKIIFSAIGANGSGLHGDKMLTSYLPE
 ILKQSTVLALTAREPLNYFLLLRALFRSIGGGAQDILYGKFLQLLPNLLQFLNKL
 NLOSCQHRQMRELVELCLTVPVRLSSLLPYLPLMDPLVCAMNGSPNIVTQG
 LRTLELCVDNLQPEYLLNMLPVRGALMOGLWRVVSAPDTSSMTAAFRILGK
 FGGANRKLNNQPQILQVATLGDTVQSYINMEFSRMGLDGNHSIHLPLSELMRVV
 ADQMRYPADMILNPSPAMIPSTHMKKWCMELSKAVLLAGLGSSGSPITPSANL
 PKIIKKLLEDFDPNNRTTEVYTCPRESREL FVNALLAMAYGIWNKDGFRHVYS
 KFFIKVLRQFALIGVLEYIGGNGWMRHAEEEGVLPLCLDSSVMVDALIICLSETS
 SSFIIAGVMSLRHINETLSLTPDIDQMSKVPMCKYLMKVFKLCHGPAWYARS
 GGINAIGYMIESFPRKFVMDFVIDVDSIMEVILGTVEEISSGSADSAYDCLKKM
 MRVYFIKEEGQEEENLTATIFVSAISKHYFHSNERVREFAIGLMDHCMVHSRLA
 PSLDKFYRFKEFFEPELMRVLTTVPTMSLADAGGSLDGVQNYMFNCPDGFDF
 EKDMDMYKRYLSHLLDIAQTDFTLNQORNAFKKCETCPSHFLPPFPITTHIDSMR
 ASALQCLVIAYDRMKKQYIDKGIELGDEHKMIEILARSSKITVDQVYESDESWR
 RLMTVLLRAVTDRETPEIAEKLHPSLLKVSPISTIIATFGASYIRNISGAGDDSDS
 DRHISYNDIMKFKCLVELNPKILVTKMAVNLANQMVKYKMSDKISRILSVPSSFT
 EEELDDFEAEKMKGIREDMIGHTVKMLAGCPVTTFTTEQIIVDISRFAAHFEYAY
 SQDVLVNWIDDVTILNKSPKDVWKFFLSRESILDPARRSFIRRIIVYQSSGPLRQ
 EFMPTPEYFEKLIDLDDEENKDEDERKIWDRDMFAFSIVDRISKSCPEWLSPNS
 PIPRIKKLFSETEFNERYVVRALTEVKKFQEEIIVKRMTEHKYKVPKLILNTFLRYL
 RLNIYDYDLFIVIASCFNGNFVTDLSFLREYLETEVIPKVPLQWRRELFLRIMQKF
 DTDPTAGTSMQHVKALQYLVPTLHWAFFERYDTDEIVGTAPIDDSDDSSMDVDP
 AGSSDNLVARLTSVIDSHRNYLSGDMVIVFYQLCTLFVQNASEHIHNNNCKKQG
 GRLRILMLFAWPCLTMYNHODPTMRYTGFFFLANIERFTINRKIVLQVFHOLMT
 TYQODTRDQIRKAIDILTPALRTRMEDGHLQILSHVKKILIEECHNLQHVQHVQFQ
 MVVRNYRVYYHVRLLELLTPLLNGVQORALVMPNSVLEKFSWQTRRHAVEICEMV
 IKWELFRTLKTDHIIISDEEALEVDKQDKLRTASSTDRFD FEEAHNKRDMPPDAQ
 RTIIKEHADVIVNMLVRFCTMFHQNSGSSSTSQSGNHGVELTKKCQQLLRAALR
 PSMWGEFVSFRLTMIEKFLSIPNDNALRNDISSTAYANTIONAQHTLDMLCNIIPV
 MPKTSMLTMMRQLQRPLIQCLNNGAQNFKMTRLVTQIVSRILLEKTNVSVNGLD
 ELEQLNQYISRFLHEHFGSLLNCRNLSGPVLGVLGAFSLLRTICGHEPAYLDHL
 MPSFVKVMERAAKEHLAYVANSQDGNMVKNFFPDVAELLCACMELVRPRVDHI

FIGURE 10

SMEIKRSIVGGIIAELIISNHDKIIQTSVKLLGAMISTQDMEFTILTVLPLLVRIOISII
VTKFKNCKDLIADYLVVVITVFENSEYRNSEAGSRLWEGFFWGLKSSDPQTREK
FSIVWEKTWPHMATVDIAHRMKYIMQNQDWSKFKHAFWLKFALWGMLRTIAKR
PTDPNNKRKKVILLNCATPWRTIEYAAKLKDQPMEVETEMKREEPEPEVDEK
DSQDDSKDAGEPKEKEKLTLELLLAGOQELLDEASNYDFADALDTV SQITFALN
ENQVTSKMWWVLFSFWSSLSQSEIEDFTALVVPFMSSGVHNNYQTGVQDSV
LAVWLEAVGDAVHLPSRLIEFISSKHECWHTGIRLLENHIWTIPKQLNNTLLREM
KVAPGLAGDIETLES LGTLYNEISEFDQFAAIWERRAVFPDTMRAMSAMQLGD
MELAQSYLEKSMSSTYETLAPTINPNNTSNSEKHVSPIIDKEYDHWMEMYITNC
SELLQWQNVADV CNGKDMQHVRGLINAASHIPDWNVVEECKSQIAGCIPPSFH
LDYTLFNL MSTVMRMNENSSPT HMKERCKIAIQECTEAHISRWRALPSVVSYG
HVKILQAMNLVREIEESTDIRIALLEAPSNKV DQALMGDMKSLMKVFRNRTPTTS
DDMGFVSTWYDWRNQIHGMMLQRFEYWDKVGLNVAATGNQSIVPIHSMAQA
QLAVAKHAKNLGFHNLTKDLLNKLAGLTAIPMDAQDKVCTY GKTLRDMANSA
ADERVKNELLCEALEVLEDVRIDDLQKDQVAALLYHRANIHSVLDQAENADYTF
SAASQLVDLQNSVTTTGIKLMKNWGHHL YKRFFSTTVCKETGN NFGQALACY
FIAARVDNDIKARKPIAKILWLSKHLNACGSHEVMNRVIKKQLHSLNLFNWLYWL
PQLVTDVRYKPNSNFVLILCKMAAAHPLOVFYHIREAVSVDDIDSVLEEDYTDEQ
MSMDVSD EDCFADDPFDRILKICLK YRPTDIRVFHRVLKELDEMNETWVERHL
RHAICLK DQMFKDFSEQMDATFNEMQYSEDVTMMTLRWRKQLEEDLVYFQQN
YNLDFLEIRNKRKMIVTKGCMGVEKSQIMFEKELS QVFTEPAGMQDEFDFVTN
MTNMMVSQLDIHAVDAPRPQGYIRIVLDWIRAIRRRFDRLPRRIPLESSSPYLAR
FSHRTGCIEMPYDLLNVLRAKNHTLMASNQTGQYISMLSRFEPNFEIVIKGGQVI
RKIYIRGQTGKSAAFYLKKSVD EPTNRVPQMFKHLDHVLQTDRESARRHLHA
PTVLQMRVGQKTTLYEVASVQPYAMP PDCTRNYPASQIDIVHPYDVL TATFNG
SYYPDDMVLHFFERFAQSSSSIGQPLPTPTNQDGT VAPPRLTEAHHIKNIIYEDF
ARDMIPFRLLYDYLTARYPD PVMYYAMKKQLLHSLAVLSTIEYHCNLT PMGPDQ
MMMTMNTGVLSNPSYRFEIRGGRSLHDIQHF GHEVPFRLTPNLSILVGVAQDG
DLLWSMAAASKCLMKKEPEVIMRPLWDEFANNTDCDKSRLQVFACHASNSYI
NGVASKLRNTNSADAKLRKDDCVSLISRAKDS DN LARMPPTYHAWF

FIGURE 11

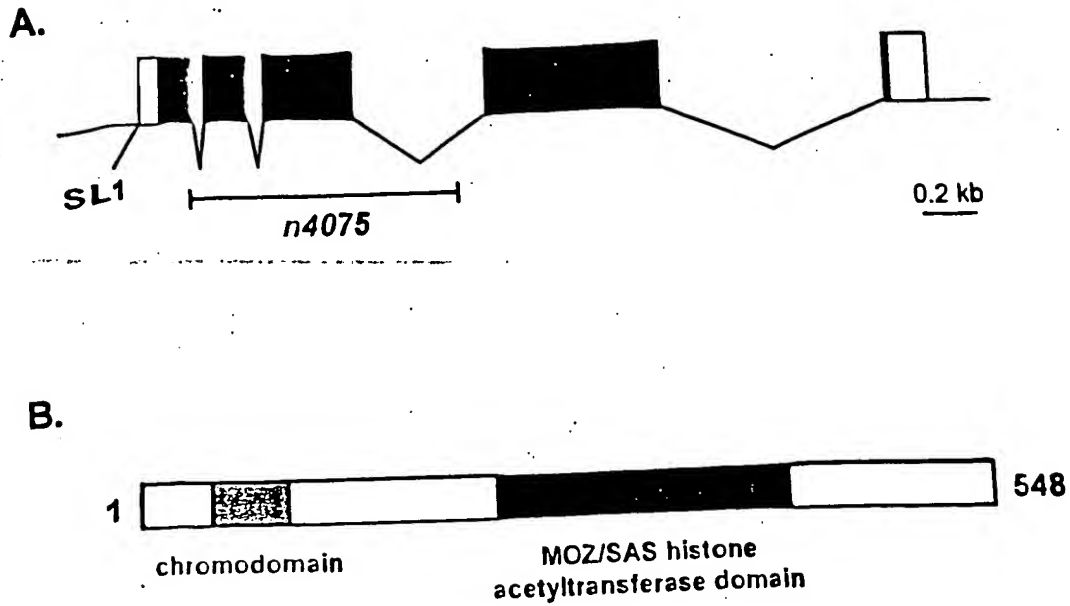


FIGURE 11B

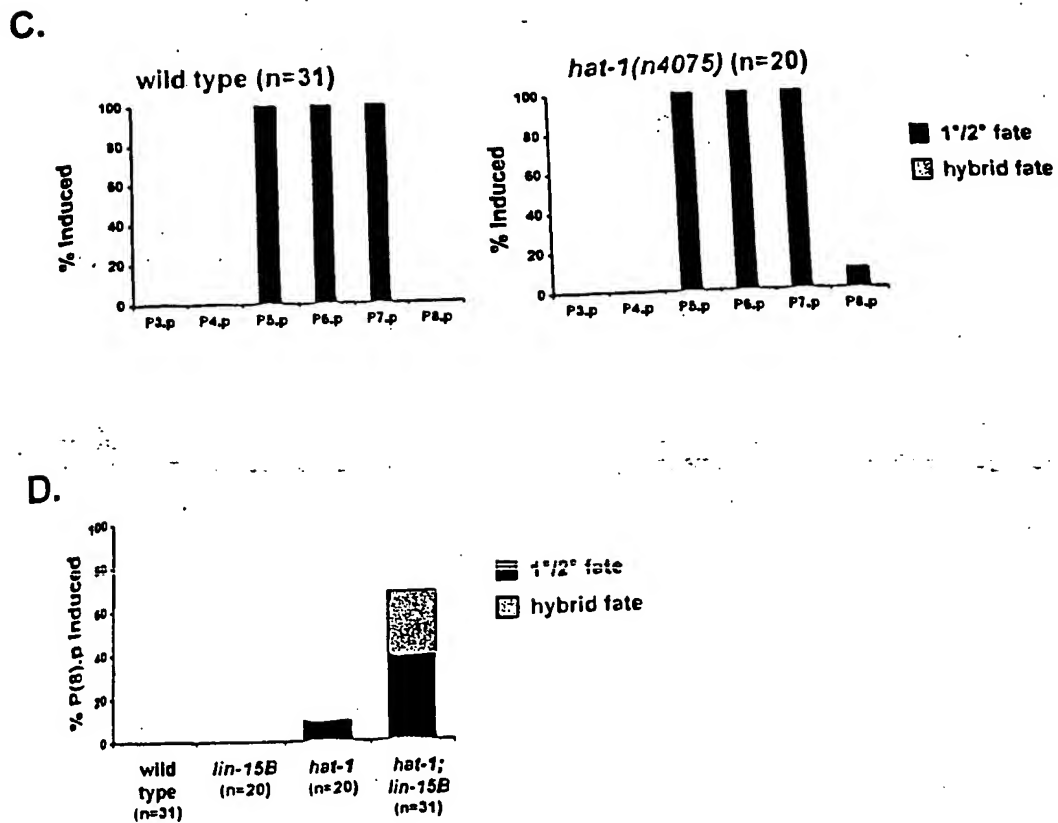


FIGURE 12

hat-1 genomic sequence

TTGTTTTCGGATTTTTGTGTGCTTCGTAGTTGCTCCGATGATGCCGGATT
AACATTTGAATGTAACATTTGAATTTTGAATTTGAAGGAATTCATTTGAATCTA
AAGCTTGCAGGGTCAAGACCGATACATTCTTGCAACACATGACTCGAAAGTA
TGTAAGGAAAAATTGAAGTTGGAACTTGAATTTGATGAAAAAGTACAGTAA
TCCATTCTCTCTTATTTTCGCAACTTTCTTCGATTTTTGATTTTTCCTAGATTTT
TTAAGCTAAAATTTTGTGTTTTATTTTCATTTTTCATGCTTTTCAATTTTCGGTT
TTCAACAAAATTATGTTTTTCAGAGAAAATCTCGTGAACAATAACTCGGCTAC
TGTACCATTTAAAGGCGCACACCTTTTCGCGCAGCATTGATTTAAATTTTTT
GTTCTGGCTCAACAGTGCAATGGACATCTAGATATCTGAAATTTTACCACT
GAATTCAGTTCAATTTTTAAGCATCTTCAAAAATTTGCGTTTTCTTAATTTCT
TGTGATCGTTTTTTTTTGAAGTACAATCGTACATTATAAATAACTATTTTCT
AATTCGAATAATTTAATTCAAGATCATTTTCGCAAAAATAATTGCCTTGAAACGT
TATGCCGCGGTCAATTTTCAACCACCCTTGTTATTCTTTTTTGAATTGCCGCC
CTTTTTCCCTGTGGCCGGCGCAGTGCGGCCGAGGTTGGTTTCTAGGCCAG
CCGGCGCGTTTTATTTTTTTCGAGCATGATTTTCACAATTATTTCTTGCATTTT
AAAGTTTTTTATTGATAAAATAGTAAACTAACAACGGATAATATTATTTAAA
ATTAAAAACTAGTTTGTTCATTTTGGATCGATTTTATAGATGTTGTTTCATGGA
TTATGCACGCAAGAAAGTACTATCGTTCACATTTGATTGCTATATTATTGAAT
ATTGAATTTTTCACACAAAATTGTACTATTTCCAGATATTTATCATGACCGAG
CCGAAGAAGGAGATTATAGAGGACGAAAATCATGGAATATCCAAGAAAATAC
CAACAGATCCCAGGCAATACGAGAAAGTTACAGAGGGATGCCGGTTATTGG
TCATGATGGCTTCAACAAGAAGAAGAAAGTTAGTTTTTACATCTATTTAAACAC
ATTTTCCAATTATTTTCAGGATGGGCCGAAGTTATTTCAAGATGCCGAGCTG
CAAATGGTTCAATTAATTCTATGTCCATTATATCGATTGCAACCGAAGACTT
GACGAATGGGTTCACTCTGATAGGCTCAATTTAGCGTCTGTGTGAGCTACCA
AAAAAAGGAGGAAAGAAAGGAGCACACTTGCGGGAAGAAAAGTGAGAAATC
TATAAACTTTTCAAAGATTTTAAATAGTTTTATCAATTCATAATTATTTAGTC
GAGATTCGAATGAAAATGAAGGAAAGAAAAGCGGCCGAAAACGAAAGATTC
CACTACTTCCGATGGATGATCTCAAGGCGGAATCCGTAGATCCATTACAAG
CAATTTCAACGATGACCAGCGGATCTACTCCAAGTCTTCGAGGTTCCATGTC
GATGGTCCGCCATAGTGAAGATGCAATGACAAGGATCCGAAATGTCGAATG
CATTGAAGTAGGAAGATCACGAATTCAGCCATGGTACTTTGCACCTTATCCA
CAACAATTGACAAGTTTGGATTGATTTATATTTGCGAATTTTGTCTGAAATA
TCTAAAGTCGAAAACCTGTCTGAAACGGCACATGGTGAGTGTTTCGAGTTAT
AGAAAATGACCGAATATAAATAACTGTTTTCAAATTCAAAATTTTCAATTTT
CCAAAATGAAAGAATCGGTGAATTCGAAAAAATTCGAGTTCTTGTGTGTTTT
TGGCTGAATTTTTCGGTTTTTCTTGCTTTTTCCGTTGATATTAGTTTTGAAACA
TCCAAAATTCATTTTTGAAATACTTTTTTGCGAAAACGAAAAAAAATTC
CAAACGGTGTTTCAAACCAAATTTATCGTAATCAAAAAAGTTTCGCAAATAGG
CCATTATTCTGCGTGGGAATTCAAATTAATCAGCTACTTTTTCTATTTTGC
AAAATGGAAAAAAACGTAAAAATAGACAAATTTTAAATTTTTAAACAATTA
CATTCGGTCCATACTCTTCATTTTCTATCATTTAATTAAAATGCCCAATTCTAA
TTAATTTTATTTTCAGGAAAAATGTGCAATGTGTCAACCCACCTGGCAATCAAAT
CTACAGTCACGATAAACTTTCAATTTTTTGAATCGACGGCCGCAAAAACAAA

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING

Applicant(s): Horvitz *et al.*

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FIGURE 12

AGCTATGCTCAGAATCTATGCCTGCTTGCCAACTTTTTCTGGATCACAGA
CTCTTTACTATGACACGGATCCATTTTTGTTCTATGTGCTAACCGAAGAAGA
CGAGAAGGGTCATCATATAGTTGGATACTTTTCAAAAGAAAAGAATCAGCT
GAAGAATATAATGTTGCGTGTATTCTTGTGTTACCTCCATTTCAAAAGAAAG
ATACGGAAGTTTGCTCATCGAATTCAGCTATGAACTCTCGAAAATTGAACAG
AAGACAGGATCACCCGAAAAACCACTATCAGATTGGGACTTCTCTCATATC
GATCGTACTGGTCAATGGCCATCATGAAAGAGCTTTTCGCATTCAAAAGACG
ACATCCAGGCGAAGATATCACAGTTCAGGACATTTACAAAGTACATCGATT
AAACGAGAAGATGTTGTGTCAACGTTACAGCAACTTGATCTATACAAATACT
ATAAGGGATCATACATAATTGTGATTAGTGATGAAAAGCGTCAAGTTTATGA
GAAACGGATTGAGGCTGCGAAAAAGAAGACACGAATTAATCCAGCAGCTCT
GCAATGGCGACCCAAAGAGTACGGAAAAAGAGTGAGTTTTTTTTCAATCA
AAAATTCGTGTTTACGGCTAAAAACTGAAAATTAATTAATTAATTCGTG
ATAACATTTTTTTTTCAAAAAACCAAAAAAACAATTCGTTTTTGGCAGAAC
CAAAAAAAAATTTAAAAAAAACGGTTTACGCCCTATTTATACAAACAACA
GAAATTGCACTTTTTTGAAGCAATTTGACCCTACAATTTTTTCCAGTTTTTG
CTCTTTTTCAAAAAAACAACCTAAACACTGGAAATACTAAATACTAAGGAAA
AAAATGGAAATACTGTTTACAGTGTCAAAAAATTGAAATTTCTAATAAAAT
CATTTTTCTTTTTACTAAATTTATCAAAAATTTATAACTCAAATCTTTCAGTTTT
TGCGAATTTTTTTTCGAAAAACGAAAAAAATAAACCTAATTTTAACCAAATT
GTAATTTTGAAAAATCTGGAACGTCCGGAAAACTGAAAAATTAAAAAAAAC
TTTTCAGAAATTTATTTTTAAAAAACCGTTTTTTTTAAATCAAATTTGTATATGT
TGATGAGAAAAAAAATAGAAATCAATGTTTTTAAGTTTTAAAAGAAAAATTTA
TTTTAATTATTTTAGTTTTAATAAGGTATTTAAACAGTAACAAGGATGTCCGGT
TTTCGATTTTCCGAAAAACTAAAAAATTGTCTTTTCGATTTTTTAATCGAAAA
AAAATAGAAATATTTTACAAAACATACTATTCTTCTAAAAAAAAGAATAGTG
GGAGATTTTAAATAATTTTTGAAGTCTCGCAATTTTTTTCGAAATATCGAAAA
TCGAAAAACCGGCACAAAAGCAAAAAGTCTCCGGGAATATATCTTTAAATTA
TTTTATGAAGTTTTTTTTTTCAGGCGCAGATCATGTTCTAGCAACAACGACATGT
GTTCTCGCCACGACGATCTCAACCTGTACATTAAAAATAACACTCCGTTTTTA
TCTCGCATCTACACACCGAAAAGCTTACGCTATCCCTTTATCATTCCCACAC
CGCTCAGAGAGCGTACGCCTCATTTTATTGTTCTGTGTAATAATTTG
ACTTATTAGTCACTTATTTTTTTAATGAAATTATTCTTGAATTTTATAATCTTCT
TGTTGCAGTTCAAATAATTAATAATTCATCATATAGACAAGTAAGTTTATAACT
GCAAAAGTGAAGTTTTCTAATCATTAAAGCGTTCTGAAGATATTCGGCAACCG
CCTGAGCGATCAGATCACGGCGGGAACGAGTTGAGGCGTAGACATGCTTG
CAGCCAGTGACAACCTGAAAGATATTCAAAAAATTAATTTCAAGGACTCGAAT
TTTTAACAATCTGAATAAAAAAATCCAAAATTGTATATTATAGAGTTTTTTGAA
ATCTAAGCGAAAGCGCGCTCCAATGTAAAACGAAAAGTGCTCCGCCCTAA
ACGTTGGGTCCCGTTAGGAATTTGTTATTTTTTCGGTTATTTCTGACTATATT
ATAATTTGAAACGACAAGTATTTTAAACATCATTTGACATAAAAAATATGT
AAAACAACAAAAACAATCGAAAAAATAGTGAAAAAGTTTGAATTTACAGTCT
CGCCGCCTCCTACCGAGACCTAACGTTAGGAGGCGGAGGGTTTTCTTTGG
CATTGAAGCGCGCTTGCTGCGGCCCATTAATAACTTACAGCCTTTGCA
AAGTCCTTCTTCTGTTTATCCTCAATCTCGTCAATGTATTGATTGGACAACCT
CTCAATCTCGGACTGTTCCGCATTTTCATCCTTCAATTTTTGTATTGAGCCT

FIGURE 12

TGAATTGAGCCACCTTCTCCTCTCCGAAAGCCTTAACCGAATACTCCTTACA
AGCTTCTTTCAACTTGCCCTCGGCCTTCTCCTTGGCATCTC

FIGURE 13

hat-1 ORF

ATGACCGAGCCGAAGAAGGAGATTATAGAGGACGAAAATCATGGAATATCC
AAGAAAATACCAACAGATCCCAGGCAATACGAGAAAGTTACAGAGGGATGC
CGGTTATTGGTCATGATGGCTTCACAAGAAGAAGAAAGATGGGCCGAAGTT
ATTTCAAGATGCCGAGCTGCAAATGGTTCAATTAATTCTATGTCCATTATAT
CGATTGCAACCGAAGACTTGACGAATGGGTTCACTGATAGGCTCAATTTA
GCGTCGTGTGAGCTACCAAAAAAGGAGGAAAGAAAGGAGCACACTTGCG
GGAAGAAAATCGAGATTGGAATGAAAATGAAGGAAAGAAAAGCGGCCGAAA
ACGAAAGATTCCACTACTTCCGATGGATGATCTCAAGGCGGAATCCGTAGA
TCCATTACAAGCAATTTCAACGATGACCAGCGGATCTACTCCAAGTCTTCGA
GGTTCATGTGATGGTCGGCCATAGTGAAGATGCAATGACAAGGATCCGA
AATGTCGAATGCATTGAACTAGGAAGATCACGAATTCAGCCATGGTACTTTG
CACCTTATCCACAACAATTGACAAGTTTGGATTGTATTTATATTTGCGAATTT
TGTCTGAAATATCTAAAGTCGAAAACCTTGTCTGAAACGGCACATGGAAAAAT
GTGCAATGTGTCACCCACCTGGCAATCAAATCTACAGTCACGATAAACTTTC
ATTTTTTGAAATCGACGGCCGCAAAAACAAAAGCTATGCTCAGAATCTATGC
CTGCTTGCCAAACTTTTTCTGGATCACAAGACTCTTACTATGACACGGATC
CATTTTTGTTCTATGTGCTAACCGAAGAAGACGAGAAGGGTCATCATATAGT
TGGATACTTTTCAAAGAAAAAGAAATCAGCTGAAGAATATAATGTTGCGTGT
ATTCTTGTTACCTCCATTTCAAAGAAAGGATACGGAAGTTTGCTCATCG
AATTCAGCTATGAACTCTCGAAAATTGAACAGAAGACAGGATCACCCGAAAA
ACCACTATCAGATTTGGGACTTCTCTCATATCGATCGTACTGGTCAATGGCC
ATCATGAAAGAGCTTTTCGCATTCAAAGACGACATCCAGGCGAAGATATCA
CAGTTCAGGACATTTACAAAGTACATCGATTAAACGAGAAGATGTTGTGTC
AACGTTACAGCAACTTGATCTATACAAATACTATAAGGGATCATAcataATTG
TGATTAGTGATGAAAAGCGTCAAGTTTATGAGAAACGGATTGAGGCTGCCA
AAAAGAAGACACGAATTAATCCAGCAGCTCTGCAATGGCGACCCAAAGAGT
ACGGAAAGAAAAGAGCGCAGATCATGTTCTAG

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING

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FIGURE 14

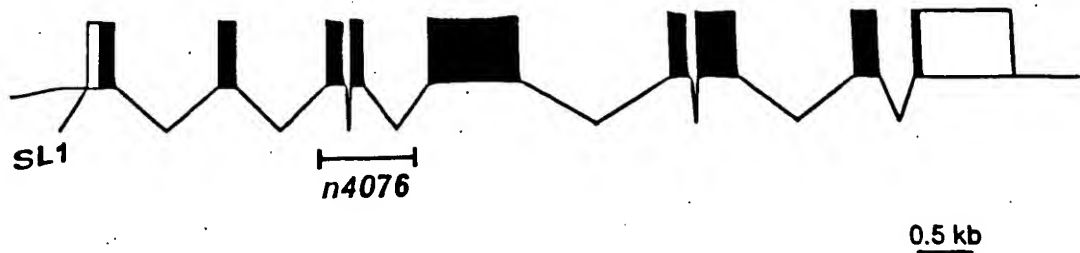
HAT-1 protein

MTEPKKEIIEDENHGISKKIPTDPRQYEKVTEGCRLLVMMASQEEERWAEVISR
CRAANGSIKFYVHYIDCNRRLEWVQSDRLNLASCELPKKGGKKGAHLREENR
DSNENEGKKSGRKRKIPLPMDDLKAESVDPLQAISTMTSGSTPSLRGSMSMV
GHSE DAMTRIRNVECIELGRSRIQPWYFAPYPQQLTSLDCIYICEFCLKYLKSKT
CLKRHMEKCAMCHPPGNQIYSHDKLSFFEIDGRKNKSYAQNLCLLAKLFLDHKT
LYYDTPFLFYVLTEEDEKGHHIVGYFSKEKESAAEYNVACILVLPFPQKKGYGS
LLIEFSYELSKIEQKTGSPEKPLSDLGLLSYRSYWMAIMKELFAFKRRHPGEDI
TVQDISQSTSİKREDVVSTLQQLDLYKYYKGSYIIVISDEKRQVYEKRIEAAKKKT
RINPAALQWRPKEYGKKRAQIMF

FIGURE 15

A.

epc-1



B.

ssl-1

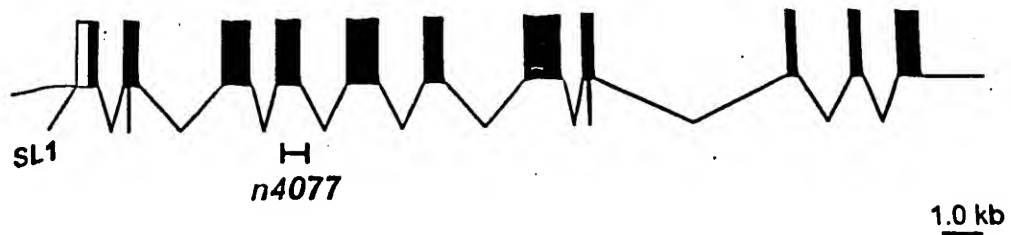


FIGURE 16

epc-1 genomic sequence

TTTCAAAAAAAAAAATTACCTCGTCAATTTCACTCTCCTCGATGCGATGATT
 ATCCTCGTCCATTTTACCTGAAAAGTGTGATTTTTTACGAATAAAATTATTTT
 CAGATACTTCTAGAAAAAACTGAACGGAATGTTACGAAATTAATTTTCA
 AAGTTGCGAACTGAATTTTCGACAAAAAGTTTCACTGATATTCATTTCAAGC
 ATATTGCAACGTTTTTAAATTAATTTCTAAGAGAAAAAACTGCAAAACAATTC
 GAAAATAATTTTTACAAGTTACTTTTCGAAAAAGTAACAAAAATCCACTAATG
 AACAAGAAATTTTTGAACAAAAAGAGCTTCTCAGGCTATTTTTGGACGAATAT
 TTTAATAAACTTTAAAAAATCAACGAAAATCCCCTAAAAATCGCTGAAAAT
 TCCAAAAATTAAAGTTCATTCTCGACCACACCTCTCGTAAATCAGCACGAGA
 CTCACGCAACGCGACCGCGCCGCACTCAACGGCATTGAGTAATGCGGGAGC
 GGCAGCGTCGCGTCGTCTATTTGTGTGTGTGTGCGATTGTGTGTGGTGCGA
 CGTGGCCGCTCTGTGTGCCTCTCTAGTGAGTGTTTTCCGACGAGAGACAAC
 ACATTTTCGAGAGACGAAGAGAGTGGCGACGAGGAAGATAGTGTGGTAAGA
 GGAGAGTGTGCGCGAGGGAAAGAGAGCAAAGTGTGAGTGTCTGTGAGAAG
 AGAAGGAGACCCCCCCCCCGCGCTCAACCAAGTCGATAGTTGGCCTGA
 GTGTAGGGCCTTCTGTTGTATTCCACTGCTAACCCCCCCAAACACACAAAA
 AGACTCAAAAAGTACTGCTTAAACACAGTGCTCAGCTCATTTTCATTTTGAT
 TTTTATGCTCGCCGTCATCGGCGGATGAATTCATCGCAAAGTCCGTGGCGA
 TTCAACACGTGCGGCGTCTCGCCGCTCTTCTTAACCGTAGTTACAACGTG
 GGAGTACAGAAAGATGGCCACTACTTCGAAGGCGTTTCGAGCCCCGGGCGC
 TCGACTCGAACCGGTCTATGACTGTATACTGGGGCCACGAACCTCCGGACC
 TATCAGAATGCAGTGTTGGAAACCGGGCGGTGACACAAATGCCGTCTGGCA
 TGGAAAAAGAAGAAGAACAGGTTGGTTTTTGGTGGATTATGGATTACTGCTC
 CATTTTGAAATTTTCGAGTTTTAATGTCTTTTTTCGAATTCCTGGTGCTTTTT
 TCTATCCGAATCATGTTTTAATTCGGTTTTCCGACTACTTTGAAGAATTTTCA
 AATTTTTGATCCCTGATGACGTCCTATTTTTGTCTTTGCCTTTCTGGATCGC
 TTTTATAGTTATTTTCATTTTTTATTTCTTTTTTACACTTTTAACTTAACAATTC
 TCTTAATTCATCCTATTCTATTTAATTTAAGTTTTGATTTTTGATTTTGATT
 TTCTCTTTTCTTTTTAGCCGCCGGTGGGCCTTTATTACAACTCTTAAATCAT
 AAAAAAATCAGTTTAAGCAGTTATACATAACTCTTATTATGAAAAAATCGTTA
 TTTTCGACGGAACTTCATACTTTGAATTTATTTCCAATTTAGATTTTATTTT
 CTCAAAGTCAGCTCAATTAACCTAATTTAAATGTTTTGTCCTACCCGCAAAAT
 GTTTTTTTTTAATATTTTAATTTCTATTTTAATTTTTGGCTTTAAAAAATCATTTT
 GCTAAGCCTGAGATGAAGGCGAAATCTCGAGAAAAAGCATTTAAGTAAT
 AAATTCGGTTAAAAACGACTTTTTCTATCACAGAAAGTGTCTCTGAGTGCTA
 ACAACCTTCTTCTGTCCAAATTTTGACACAATTTCCCAATTATGCCGACTTAT
 TACACCTTTTTCCGTCAATCTTCTAGTTTTTCCCACCCTCTTGACCCCTGGTG
 ACGTCATTTGTTTGTTCTTCTTCCAAGACATGCCCTGTGGGGTATTTTTTCTC
 AAAATTTTTGCAAATTTATTGGATTCTAAATAAAATCCAGGAGTCTAGCACC
 AGGAATAATAATGCAAATTTGAAAAAAAATTAACAGAAATAATGATTTTAA
 ATGATTATTTAAATTTTAAATTTTAAATTTCCAGGAAAAACACCTGCAAGAAG
 CGATTGGTGGCGAGGAAGGAGTAGATCGGGTATTCAGCTGAACCATGTCA
 TTCCAACCTCAAAAAGTCGACCGAGTCAAGATCAACGCTATCACTCCACTTA
 TCACAACAAGAATAAAATGCACCGTTCAAAGTATATCAAAGTTCATGGTGAG
 TTTTTTAACCAAAATTTCCGGCGAAAATAATTTAATTTCCGGTTTTTTGAAATT

FIGURE 16

AATTTCCGCTTGGGTTTTCTTGATTTATTATTTTTGAAATTCCTCTCTGAAT
 TCGAAAGAAAATAACTTGATTTTTAGACTTCTGGCTAAAACCTTCAAAAAT
 GTTTGTTGATTGGTTCCAAATTTTCGCCTGATTCCGAATTTGATGTGACAAA
 TTCAAAAAAAAATTCCTGATTTTATATTCAAGCTTTGTGTTTGTGTGTTCTTT
 TTGGAGCGCGCTTGCATCGTTTGATTTTCTTCGTCTTTTTTAAAATTTATTTTC
 GCTTGTTTCATTCATTTTGTTCGAGTTTTTTCTGCCAAAATGAATGAAACTG
 GTTTAAAAAATTGAATTCGGCGAAAATAAATTTTAAAAACGAAACAAATCAA
 ACGATGCAAGCGCGCTCCAATGCGATTTTTTTGGGCGCGGAAATTCGTGAT
 TTCAAGCTTAAATATAAAATCAGGTATATTTTTTCGACTTTTTTACGTTGAAA
 TTCGGAATCAGAGGAAAATTTGAGTCAATCAAAAATATTTCCAGATTTTCG
 GTATCTTTAATGCATCAAAAATGAACTTTCACCCCATACTCCAGAAAAATA
 AGAAAACAAATTGCGAAATATTGTTCCCTGATCAAATTTTTCTTTTTTAACT
 ACACTTCTCTGTTTTGAAGTGAGAAAGTACATTTTTCTGCGTTTCTTATCAGT
 TATCATTGAAAAGGATCAGAATTTGATGACGATATATTTGTTTAGTTACCTC
 CCTTTTTCTGAACAGTTTTTGGGAAAAAGGAGAAAAACCGGAATTTTCTAT
 GAAAATGTGATTTATTTTCAGCCTGGCAAGCACTCGAACGAGACGAACCCG
 AGTATGACTACGACACAGAAGATGAAGCATGGCTATCAGATCACACTCACAT
 TGACCCGCGCGTTTTGAAAAGATATTGACACAGTGGAGAGCCATTATC
 GGAGACACAGATCGCGAGCGAAGATTGGTGATTAATTTGCATAAATGTAA
 GTTGACGAAATTTCCATTGAAACCCCCCCCCCAAAAATATCGTTTAATTG
 CAGCACTGGACTCATCAATCGTGTACGAAATATACGAATATTGGCTGTGAA
 GCGAACATCGGCTGCGACGACGTCTGGTTGTGTTGGAGTCGGTGGATTAAT
 TCCGAGAGTCAGGACAGAATGTCGGAAGGTAAGAATTTGACTATTTTGAAC
 GAATTTCTGTGATGAACTTCTCTAAACTTTTTAAAGTTTTTATGGCGGTTCA
 AAATTTGCGAAAATTTACACTGATTTTAGCTAAAAACTTGAATTTTGGTCATTT
 GTCCGTGTACATCTGTCCGAAATCGACTTTTTTTGGAATTATCATCCTTTAT
 TGCACATTTGGCTAGTTTATCTCATTAAATTCGTTGATTACTAAGGTACATTT
 AAAGCCAATAGGTAACCAACCAAAAATATCATAATTTTCTACACTTTTTAA
 TTTCCGACACTACTTGAATAACCCCATAGTGACCAATTTTGATAGTTTTTG
 GCTGGTTACCGGCTTTAAATGTACCTTATTAATCAACAAAATTAATGAGATA
 AACTAGCCAAATGTGCAATAAAGGATGATAATTCATAAAAAAGTCGATTTTG
 GACAGATGTGACACGGGCAATGACCAAAATTCAGTTTTTAGCTAAAATCA
 GTGTATTTGTTTCGAAGTTTTGAACCGCTATAAAAAAATTTTTGGAATGCTTT
 TGGCAAGTTTCATTACGAAATTCACCTCATTTTCTATACGCAAAAATTAGAATT
 TTCAATTAAAAATTCATTTTACAGGATGGACAAGGTGTTATCAATCCGTACGT
 TGCATTCGGTCGACGTGCCGAGAAAATGCAGACTCGAAAGAATCGGAAAAA
 CGATGAAGATTCGTATGAGAAGATTCTCAAGTTGGTACATGACATGTGCGAAA
 GCTCAACAGCTCTTCGATATGACTGCCCGACGAGAAAAGCAGAAGCTCGCG
 TTGATTGATATGGAATCGGAGATTTTAGCGAAACGAATGGAGATGTCAGATT
 TTGGTGGTTCTCCGAGTTCGTTCAATGAGATCACCGAAAAGATTGAGCAG
 CAGCAACGTTGGAAGTCGTGAAACCACCACTGGCAGAAATCAACGGATCAG
 ATGAAGTGAAGAAGAGGAAGAAGCCGAGACGAAAGATTGCTGATAAGGATT
 TAATATCGAAAGCCTGGCTTAAAAAGAATGCAGAAAGTTGGAATCGGCCGC
 CGTCGCTCTTTGGACAACACAGTGGAAATGTTCCGACGGTTACAACGAAGC
 CAGTTCGAGAGTCGTTGGCGAATGGGCGATTTGCGTTCAAGCGGAGGAGA
 GGATGTGTTTATCGCGCGGCTCTCACCGTTTACAATGTGCCTACAGCGCCT

FIGURE 16

GCTACAGTACCTCCAGTACAGACTCAAGCAGCAGTGGCTTCATCATCATCG
TCAAAATCAACGGATATGGTGCCGTGCAACATGAAGTTCTTTGAAACTTTTG
TTCGGGATTACAGGATTCAGTTTCTCGATCTCTTGGCTTTGTACGCCGAGC
AATGGGACGAGGTGGGCGAGTTGTATTCGATCGGATGCCTCGCAATCGAG
ACGACAACGACGAACGCACTTCGACAGATCCATGGGCCGAGTATTGTGTGCG
CGGATAGTTCAAGGTGAGATTTTGAATAAGAATCTTAATTTACGAGATTTT
GGTTTTTTTCGCTGCTTTTTCTGTAATTTTGTGGTATTTTTCTCGTATTTTCA
ATTA AAAAACGGGTTTTAAATAATTTTAACTGAAATTTGCTAAAAACCAAG
AAATTTCAATTA AAAAATGCAACAAAAAAGACTGGAGGCACCACCGAATG
GAGAACAGGAGAACCCAAAACACGCCCATTTTTCCGTGCCGGGGCGGCGA
AAATTTTTGCAGAATTTGCTGCAATTTTCGTTTTACAAACGAAACAACGAAG
CTCTGAATGTGTTATTTCCGAGCTTCGTTGTTTCGTTTGTAAAACGAAAAATT
GCAGCAATTTCTGCAAAAATTTGCGCGCGGCACGGAAAAATGGGCGTAGTT
TTAGGTTCTCCTGTTCTCCTTTCCGTGGTGCCTCCAGTCTTTTTCGCATTCTT
AATGAAATTTCTTTGTTTTTACGGAATTTAGGTTAAAATTATTTAAACCC
GTTTTTTTTCAATTGGAAATGCGAGGAAAAACCACAAAATCACAGAGAAAG
CTTTTGGATTTTTTCGCAGCTTTTTCTGTGATTTTGTGGTTTTCTCGCATT
TCAATTGAAAAAAAACGGGTTTTAAATAATTTTACCTGAAATTTGCTAAA
AACGAGGAAATTTCAATACAAATGCAAAAAAGACTGGAGGCACCACCGAAA
CCGAATGCAGCTCAGAACAGGATTTACCAAAACAGGATGCAGTAGGCGGAG
CCAATTCGCAACCACCGCATGCTTATTTGCATGCCTCGCACGTTTTTTTTT
CTCTTGAAACAATGCAACAATATCAAGGAAAAACGTGCGAGACTTGCGAAA
TAAGCATGCGGTGGTTGCGAATTGGCTCCGCCCACTGCATTCTGTTTTGGT
AAATCTGTTCTGAGCTGCATTCTGTTTTGTTGGGGCTTCCAGTCTTTTTGT
GCATTTTAAATGGAATTTCTCGTTTTTAGCGAAATTTAGGTTAAAATTATTT
AAAACCCGTTTTTTTTCAATTGGAAATGCGAGGAAAAACCACAAAATCACA
GAGATAGCGAGGCCCCACGAAAAGGGGAGCAGAACAAAAAGGGGGGGG
GGGGGCTGGCACTGTGCCAAACGCACAAACGCTTTTTATTCTTATTCAACG
CACGACTTTGTTATAACCACTCCGTTATTACGCATCGCGCGCTGTTTAGC
GTGAAAATACAAAAAACGTCGTGCGTTGAATGAGAATAAAAAAGCGTTTTG
TGCGTTTGGCACAGTGCCAGCTCTCCTTTTCGCAGATCCCCTTTTCGTGGG
GCCTCAGAGAAAGCTGCCATAAACTTTTTCTTCGCGCTAAGACCAATACCA
ATAAATCCTTGCGCCTTAATATGCAAACTATATTTTCTTCCAGAACCTTCC
GTGCTCGAAACAGTTCGCTTGGTACCGAAGAAGAAACCGATGATCTAAGCC
CGAAATCTCTGTATTTGCTCGCAGTAATCGGTTTCGCATTCAACGATGATGA
AACTGAACGGGAATGGACTTCAAGATGCCAACAAATCATCGTGGAGAGATAC
AGAGGTGGATGATGAGCTGAAAAAGCGGGAAACAACGTCTGAAAGTGAGAT
TTTGAACGATTTACCTGGGAAAATAGATTATTTGGGCCTATTTTAATTATTTA
ATTGCAGAATTTACCGAAACCACGACGAATGGAAGTACCAAAACACACACA
GAATCGGATGATAGTGAAGTTGAACGGATGGAGGTTGATGATCAAGTTGAT
GAAGCTCAAATAACTGTATCATCATCAAAGACGATGGAATGAATGGAAATG
ATAAGAACGAGGATGAAGAAGATGATGATGATGATATGGATGTAGATGAACA
TCAGACTGTGGTGGGTGTGCATCAGGAGCAGGAGGAGGAGCATCACCAGC
AAAAAGTTCCGGCATCAATGAATGGTGGTGGTGGTGGTGGTGGAGTGGTAA
AACTGAAACCGCCGCTGCAAGAATTTCCGCCCGCTTTCCGGGAAACGGAA
GAGCGGACAGAGCGGAACCGACGCCGGTTCCGGCAAAGGTAGTGAGGCTT

FIGURE 16

TTTTAAATACTCGAAAAAGAAGGAAAAATCCCACTTTTAAAAATACGAT
 TCTTAAAAATGCGAATTCCTCCAAAATGAGAACTCTGATTGGCCAGGGAGC
 TCTCATTTTGAATGGAAATTAGTCAAATGAAAAATCCCGTTTTTTTTTAAG
 TTGGATTTTTCATTTCTCGCGATTTTTCCGCGTTTCTGTGTCATTCTGAA
 TTTAACATTTAATAAATTAATAATGTCTGGAATATTGACAAATTATGCTTCAAA
 TTTTTGCGCGGGAGTTCAAAAATAATTTGGCCCTTTTTATTTTTATTTTGCA
 AAAATATATAAAAAATCATTTTAAAAATTTAGAAACATTTTTAATTTTTTAA
 CAGTTATATTGCTATATTGGGACGGTATTCTGTCAATAACTTGGTGTGTC
 GAATTTTTTTTTATTGCTTTATAAGACTCAAATTTGTCTGAAAACACCGAATTT
 ATAATGAACTTCTTGAAACTTCTCAAAAAAAGTTATGACGGCTCAAAAAA
 TGACCTAAAATTTGTTAAAATTTGAAATTTGACTTGTGCGAACGGCTGGAAAC
 AATTTTTTTTTTTGAAATCACCGTCAAATTTTGAGTATAAAATTTAATTATTTG
 CGTTTTCAACTCGATTTTTGGTATTTTCAAGTCGATGGACGGCAAGATTTGG
 TAAAAAATTAAGCCGTCCATTTCTCGCCGTCCATTGACTTTAACTACC
 TAAATCGAGTTGAAAACGCAAGATAATTGACATTTATACCCAAAATTTGACTG
 TGGTTTTAAAAAGTTAGTTTCCAGCCGCTGCGACAAGTCAAATTTCCAATTT
 TAACTATTTAGGCCATTTTTGAGCCATCATAACTTTTTTTGAGAAGTTTTT
 AAGAAGTTTCATCATGAAATTCGGTGTTCAGACAATTTGAGTCTAATAAA
 GTAATTTAAAAAATTCGACAGACACCACCTTTATAGCAATTTGAATTTTTT
 TAAACTGTCTTGAAAAATCTTGAAAAAAGTCGAATAAATCCCATTTTCT
 ATTTCTTTTTGCAGATGTGCGGAACGGTGTGCGGACTCAGATGATTGGAGA
 GAGCCGAGTGGATCACCATCAGAATCGAATTCATCAACCGAATGGGGTGGC
 TATACGCCACAAGAACAGCATGCAGTTGTTGTTGCCAACGCGGTAGCTGTC
 GCTTTCAAGGAAAAATTGATGAATGGCGTGGATGATGATGATGATCAACAAC
 CATCGCCGGCTAGAGGAGCACGAGATCATTCCATCAAAGAGTTCGTTAGTT
 TTTCTTTGCTTTTTTTTTTTTTGATTTTGAGAGCAAATTTGAAAAGTTTTACA
 CGGTTTTGAAAACTGTTGAAATTAATAATTTGTTGAGAATTTGATTTGAGC
 AAGTTTTATTTTAAAAAATTGAATTTTCAGAAAATCTGAGTTTTCTTTTTAA
 AAAATTGAAATTTTCAGAAAATCTGAGTAGCAAGAATCTTAAGATCCTTAA
 TTTCTATGCAAGAATACGTAGGAGTTTACTTTGCTCAGGAAATTTATTTTTT
 GTCAGAGGAGTATATCCGAAAAAGAACAAAAAAATGCACATTTCTCAAAC
 GCGTATTTTTTTTTCAGTTCGATGTCAACGGTAACACTGCTGGAACGGAAAA
 AGTTCATGATGCCGTGACAATCGGTCTAATAATTTGAACTCTCTGCTGCTGC
 TTCTGCTACTGCTGCTACTGCTGCTCATCGCCAATTTTCAATCCTCCTGAGA
 TTTTTGATGGTCATTCATTGTTTTGTGCATATCTCTCTCTCTCTCTCTC
 CCATGATTCTCAAATATTTCAATGTATTTACACCCCCACTCTGTCCGCTGCCT
 AATCCCCGACCGAATAATCAGATTCGCTGGAAAAATCTGCGATTCTTTAATA
 TTGCAACCACCCACCCAATAATATGTGTCTCATCATCTCGGTACTCTCACTT
 GAGCCGTGTTTTCTGTAGTATTTATTCTCTAAAAAAAATCATTTTAAATA
 ATATACGTACACATTTATATCTGTAATATATTTTTAAAAATGATCCCCCT
 CCCCTCCATTCGTTGTTTTTTTTCTGTGGGTTTCAAGCTTTGAGCTGTGAAA
 AATCTCATCCCATCATCATTTTCTATTGTTTTTTTACAGTTGAAATATCCTA
 TTTATCTTTTCTTTTTTTTTCATTTTTTTTTTTCATCGTGGGGGATTCATT
 TTTGCTCCCGCGAAACGCCCGCCGCCGCAATCCCACTCTCTCTCTCAGT
 CTCTTCTAATGATCTTCGAAACTATTTTTATTTCCCTCATTAACAATTACGAG
 GTCGTCTTTTTTTTTCCCCACCCCCCACTGTTTGGTGTAATTTTGTGTTCCG

FIGURE 16

GGAGGTTTTTTGTGTGTGGATTTTTGGATTTTTGGATTTTTCAACAAAAA
TTCCCCCGAAATCAAATTTTTTCCCATTTTCCCCTCAATATTAGTACTGTTG
TATAAATAAACTTGCTCTCTCTCTCTCTCGAAATCTCCTACTATTATTTTT
TAAAAGATTTTTCCAACAAAAATTCAAAAAACCAACAAACGACCTCTCTGCA
CGCGGTAATCCTCTCTCTTTTTGTCCCCCATTTTCTCTGTTTCTCTTTTTTCT
ATCCCCTATACCTGTGATTGGAATATC

FIGURE 17

epc-1 ORF

ATGGCCACTACTTCGAAGGCGTTTCGAGCCCGGGCGCTCGACTCGAACCG
 GTCTATGACTGTATACTGGGGCCACGAACCTCCGGACCTATCAGAATGCAG
 TGTTGGAAACCGGGCGGTGACACAAATGCCGTCTGGCATGGAAAAAGAAGA
 AGAACAGGAAAAACACCTGCAAGAAGCGATTGCTGCCCAGCAAGCCAGTAC
 ATCGGGTATTCAAGCTGAACCATGTCATTCCAACCTCCAAAAGTCGACCGAGTC
 GAAGATCAACGCTATCACTCCACTTATCACAACAAGAATAAAATGCACCGTT
 CAAAGTATATCAAAGTTCATGCCTGGCAAGCACTCGAACGAGACGAACCCG
 AGTATGACTACGACACAGAAGATGAAGCATGGCTATCAGATCACACTCACAT
 TGACCCGCGCGTTTTGGAAAAGATATTGACACAGTGGAGAGCCATTTCATC
 GGAGACACAGATCGCGAGCGAAGATTGCGGTGATTAATTTGCATAAATCACT
 GGACTCATCAATCGTGTACGAAATATACGAATATTGGCTGTGGAAGCGAACA
 TCGGCTGCGACGACGTCTGGTTGTGTTGGAGTCGGTGGATTAATTCGAGA
 GTCAGGACAGAATGTCGGAAGGATGGACAAGGTGTTATCAATCCGTACGTT
 GCATTCCGTGACGTGCCGAGAAAATGCAGACTCGAAAGAATCGGAAAAAC
 GATGAAGATTCTGATGAGAAGATTCTCAAGTTGGTACATGACATGTCGAAAG
 CTC AACAGCTCTTCGATATGACTGCCCGACGAGAAAAGCAGAAGCTCGCGT
 TGATTGATATGGAATCGGAGATTTTAGCGAAACGAATGGAGATGTCAGATTT
 TGGTGGTTCTCCGAGTTCGTTCAATGAGATCACCGAAAAGATTGAGCAGC
 AGCAACGTTGGAAGTCGTGAAACCACCACTGGCAGAAATCAACGGATCAGA
 TGAAGTGAAGAAGAGGAAGAAGCCGAGACGAAAGATTGCTGATAAGGATTT
 AATATCGAAAGCCTGGCTTAAAAAGAATGCAGAAAGTTGGAATCGGCCGCC
 GTCGCTCTTTGGACAACACAGTGGAAATGTTCCGACGGTTACAACGAAGCC
 AGTTGAGAGTCGTTGGCGAATGGGCGATTTGCGTTCAAGCGGAGGAGAG
 GATGTGTTTATCGCGCGGCTCTCACCGTTTACAATGTGCCTACAGCGCCTG
 CTACAGTACCTCCAGTACAGACTCAAGCAGCAGTGGCTTCATCATCATCGTC
 AAAATCAACGGATATGGTGCCGTGCAACATGAAGTTCTTTGAAACTTTTGT
 CGGGATTACAGGATTCAGTTTCTCGATCTTTGGCTTTGTACGCCGACGAA
 TGGGACGAGGTGGGCGAGTTGTATTGATCGGATGCCTCGCAATCGAGAC
 GACAACGACGAACGCACTTCGACAGATCCATGGGCCGAGTATTGTGTGCGG
 GATAGTTCAAGAACCTTCCGTGCTCGAAACAGTTCGCTTGGTACCGAAGAA
 GAAACCGATGATCTAAGCCCGAAATCTCTGTATTTGCTCGCAGTAATCGGT
 TCGCATTCAACGATGATGAAACTGAACGGGAATGGACTTCAAGATGCCAAC
 AATCATCGTGGAGAGATACAGAGGTGGATGATGAGCTGAAAAAGCGGGAAA
 CAACGTCTGAAAAATTTACCGAAACCACGACGAATGGAAGTACCAAAACACA
 CACAGAATCGGATGATAGTGAAGTTGAACGGATGGAGGTTGATGATCAAGT
 TGATGAAGCTCAAATAACTGTATCATCATCAAAGACGATGGAATGAATGGA
 AATGATAAGAACGAGGATGAAGAAGATGATGATGATGATATGGATGTAGATG
 AACATCAGACTGTCGTGGGTGTGCATCAGCACCAGCAGCAGCAGCATCACC
 AGCAAAAAGTTCGGCATCAAATGAATGGTGGTGGTGGTGGTGGTGGAGTG
 GTAAAATGAAACCGCCGCTGCAAGAAGTTTCGCCGCCGCTTTCCGGGAAAC
 GGAAGAGCGGACAGAGCGGAACCGACGCCGGTTCCGGCAAAGATGTGCG
 GAACGGTGTGCGGACTCAGATGATTGGAGAGAGCCGAGTGGATCACCATCA
 GAATCGAATTCATCAACCGAATGGGGTGGCTATACGCCACAAGAACAGCAT
 GCAGTTGTTGTTGCCAACGCGGTAGCTGTCGCTTTCAAGGAAAAATTGATG
 AATGGCGTGGATGATGATGATGATCAACAACCATCGCCGGCTAGAGGAGCA

Title: RB PATHWAY AND CHROMATIN REMODELING
 GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING

Applicant(s): Horvitz *et al.*

Filing Date: September 12, 2003 Serial No.: N/A

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FIGURE 17

CGAGATCATTCCATCAAAGATTGATGTCAACGGTAACACTGCTGGAACGG
AAAAAGTTCATGATGCCGTGACAATCGGTCTATAA

FIGURE 18

EPC-1 protein

MATTSKAFRRALDSNRSMTVYWGHELPDLSECSVGNRAVTQMPSGMEKEE
EQEKHLQEAIAAQASTSGIQLNHVIPTPKVDRVEDQRYHSTYHNKNKMHRSK
YIKVHAWQALERDEPEYDYDTEDEAWLSDHIDPRVLEKIFDTVESHSSETQI
ASEDSVINLHKSLDSSIVYEIYEWLSKRTSAATTSGCVGVGGLIPRVRTTECRKD
GQGVINPYVAFRRRAEKMQTRKNRKNDEDSYEKILKLVHDMMSKAQQLFDMTAR
REKQKLALIDMESEILAKRMEMSDFGGSPSSFNEITEKIRAAATLEVVKPPLAEIN
GSDEVKKRKKPRRKIADKDLISKAWLKKNAESWNRPPSLFGQHSGNVPTVTTK
PVRESLANGRFKRRRGCVYRAALTVINVPTAPATVPPVQTQAAVASSSSSK
STDMVPSNMKFFETFVRDSQDSVSRSLGFVRRRMGRGGRVVFDRMPRNRDD
NDERTSTDPWAEYCVADSSRTFRARNSSLGTEETDDLSPKSLYFARSNRFAF
NDDETEREWTSRCQSSWRDTEVDDELKKRETTSEKFTETTTNGSTKHTES
DDSEVERMEVDDQVDEAQITVSSSKDDGMNGNDKNEDEEDDDDDMDVDEHQ
TVVGVBHQHQHQHQHQKVRHQMNNGGGGGGGVVKLPPLQELSPPLSGNGR
ADRAEPTPVPKMCCTVSDSDDWREPSGSPSESNSSTEWGGYTPQEQHAVV
VANAVAVAFKEKLMNGVDDDDDDQQPSPARGARDHSIKDSMSTVTLLERKKFM
MPSTIGL

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FIGURE 19

ssl-1 Genomic

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cagctgatgt tgttgatgga aaaatgacgg ctgcaaagaa gccattggct gcaactgagc 60
caaaagtgca taataaataa atgtgtttct aggatcttct aataattttt tttctgtttt 120
ctagctctaa acttgatatt atttcattct tgttctacca aattcccacg gattctacgc 180
tttatgtttc taaattatta ttctttttta tttatatctg cattttcttc taaaaactct 240
ggtcattttc ttgttttttt cttggtaatt ataaaaatta gtcatacaaa tcttggttaa 300
tatctggcta ttcagtgaac aaaccatttt ccgctctaaa ttcgaccgca atcaatcgaa 360
aaatggctca aaacgatgcc atctggctgc aacccccctg tcgtctctca attttgtgta 420
ctctctcgca gccacgcacg cgacgcaacg cactcgctgc gcggtcgag ttctttttca 480
aatttatcgc gccatttttg ttttgctca tatttatcgg ctcacgattg attttcgctg 540
aaaaacgcgc ttaatcgatt cctttttacc tgaaaaatgt tgttccaatt ggaaaaccag 600
ttgaagatcg atgaattttc aagaaaaatca ttcaaatagg caaaaccgcg tgaactttga 660
aattcgattt ttgagttttt tgaagaaaat ataattattt catcatttat gttggctctg 720
ttggctctca gcatagaaaa ttcggacatg acattagaaa ttcataataa ctgctcccaa 780
tatcgggatt agaacgattt tcagctcaaa atatggaaaa ttggttacat aaaccgcata 840
ttttagcat taatcttgaa cagctatatg gcattaaaaa aaaatatata tatacattgt 900
ttttctctc gaagtttctc tttttgttcc taaaatccgg aatataattt aaaaaaccac 960
ataaatttca atttgcagta cgagttcccc ccgaatcaca atg ccg gca aca ccg 1015
                                     Met Pro Ala Thr Pro
                                     1       5

gtg cgt gct tca agt act cga ata agc aga cgt aca tca tca aga tca 1063
Val Arg Ala Ser Ser Thr Arg Ile Ser Arg Arg Thr Ser Ser Arg Ser
          10              15              20

gtg gct gat gat cag cca tca act tcg tct gcg gtg gct cca cct cct 1111
Val Ala Asp Asp Gln Pro Ser Thr Ser Ser Ala Val Ala Pro Pro Pro
          25              30              35

tca ccc att gcc ata gaa act gat gaa gat gcg gta gtt gag gag gag 1159
Ser Pro Ile Ala Ile Glu Thr Asp Glu Asp Ala Val Val Glu Glu Glu
          40              45              50

aaa aag aag aaa aag aca tca gat gat ttg gaa att atc act cca aga 1207
Lys Lys Lys Lys Lys Thr Ser Asp Asp Leu Glu Ile Ile Thr Pro Arg
          55              60              65

act cca gtc gat cgg cga att ccc tac att tgc tcg att ctt ttg act 1255
Thr Pro Val Asp Arg Arg Ile Pro Tyr Ile Cys Ser Ile Leu Leu Thr
          70              75              80              85

gaa aat cga tcg att cgc gat aaa tt gtacgatttt ttaaatttaa 1301
Glu Asn Arg Ser Ile Arg Asp Lys Leu
          90

ttactttcct caaatccgaa taattattag atcgcgcttc gcgtttctgc atccgcggta 1361
ttttgccttc ccactgaaaa tagcagattt atcgaatttt tagcttaaaa aaaaaatgtt 1421
ttttctgcat ttttcaaaaca aaccttttgt aaaacagtga aaatcgaatt tcaaatgact 1481
aaaatgaatt ttttttttgt ccactgggtg tggaatgggt tgaatttgaa gaaatcagcg 1541
ggatttttcg tattttctga atatttttct attaaaaatc ggtttcaaac cattttttga 1601
cttttgaata gaaaaatatt gagaaaatac gaaaaatcca gtaacttcc agcttgttca 1661
aattcaaacc attccacaac cagtggacga aaaaagttca ttttagtcat ttgaaattcg 1721
atttggtttg tttgaaaaat gcaaaaaaaa aatatttttt aaagctaaaa atttgataaa 1781
tctgaaaaaa atctgctatt ttcagtggaa aggcaaaata ccgcgaagcg cagcaagcgc 1841

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FIGURE 19

gctctaataa ttattccgct tcgagaagag cgtgtattat ttcattgtta catttcaaaa 1901
 ttatgaatta atgtttttca g g gtt ctg agc agc ggt cca gtt cgt caa gaa 1953
 Val Leu Ser Ser Gly Pro Val Arg Gln Glu
 95 100

gat cac gaa gaa cag att gct cga gct caa cgg ata cag cca gtt gtc 2001
 Asp His Glu Glu Gln Ile Ala Arg Ala Gln Arg Ile Gln Pro Val Val
 105 110 115 120

gat caa att caa cga gtc gag caa at gtatgtgaag ctgaaaaatt 2047
 Asp Gln Ile Gln Arg Val Glu Gln Ile
 125

gcaccacaaa tcaattattc taatcttggt ttacag c ata ctc aat ggt tca gtg 2102
 Ile Leu Asn Gly Ser Val
 130 135

gaa gat att ctg aaa gat cct cga ttc gca gta atg gca gat ctc aca 2150
 Glu Asp Ile Leu Lys Asp Pro Arg Phe Ala Val Met Ala Asp Leu Thr
 140 145 150

aaa gaa cca cca cca aca cct gca cct cct cct cca atc cag aag aca 2198
 Lys Glu Pro Pro Pro Thr Pro Ala Pro Pro Pro Pro Ile Gln Lys Thr
 155 160 165

atg caa ccg att gag gtg aaa att gag gat tca gag ggc tca aat acg 2246
 Met Gln Pro Ile Glu Val Lys Ile Glu Asp Ser Glu Gly Ser Asn Thr
 170 175 180

gct caa ccg agt gtt ctg ccc agt tgt gga gga gga gag acg aat gtg 2294
 Ala Gln Pro Ser Val Leu Pro Ser Cys Gly Gly Gly Glu Thr Asn Val
 185 190 195

gaa aga gcc gcc aaa aga gtgagttttg aagatagatt ggtgtgtataa 2342
 Glu Arg Ala Ala Lys Arg
 200 205

aaatgaatgt ttatatattc actgcaactt tttcctcacg agggacgagg aaaagtgggt 2402
 tctaggccat ggccgaggtg ccgacaagtt tcagcggcca tttatcttgc tttgttttcc 2462
 gctgttttc tttcgttttt catcgatttt tttcgttttt tcttaataaaa actgataaat 2522
 aaatattttt tgcagatgct aaaacaattt ccaagtaaaa aaattatgta ttcagtgggc 2582
 aagcagcggg gaaagtgggc aatgcaatat gatggattac gggaatacaa aacctaaact 2642
 ttttctgaaa catgatacat acgctgctta aatgctgaga ctacctgatt ttcataacga 2702
 gaccgctgaa aaagtgttga gggttttcaaa attcaaattt tttggtgaaa aagtcgagat 2762
 tttcgcacaa aaagtgtgaat tctgaaaacc tcaaattttt ttcagcgggc tcgttatgaa 2822
 aatcaggtaa tttcagcatc atatgtatca tgtttcaaaa aaagtgttagg tttgtatttc 2882
 ccgtaatcca tcatattgca ttgaccactt tcaccgctgc ttgcccactg aatacatgat 2942
 tttttacttg gaaattgttt tagcatctgc aaaaaatatt tatttatcag ttttattaag 3002
 aaaaaacgaa aaaaatcggg gaaaaacgaa agaaaacagg cggaaaacaa agcaagataa 3062
 atggccgctg aaacttgctg gcccctcggc catggcctag aaaccacttt tctcgtccc 3122
 tcgtgaggaa aaagtgcag tgttattgta aatctcacia gagtctggca tgatttctca 3182
 aaggcgcatg gatttattca gccctaaaat taaataaatc catacgactt taaaggtgga 3242
 gttcggaaaa tgaggatttt acttttaaat gctcaaaacta gtcccaaatg ccgaattacc 3302
 aaaaaagaaa aacggaaaaa aattcatcaa gtttgaaaaa aatgcggtatg attttgttga 3362
 aatttcaacg ctcgctaata ttcttaattt gaaccgcgct tttgtccgcg ccgcactctg 3422
 tagaattgca tccgcgctgt ttccttcctc ttccggcgcc ctacttcttt tcgattggaa 3482
 atgatgaaaa aatgagacaa aactagaatt cacgtagcgc gtcggaaatg atgaaaatat 3542

FIGURE 19

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catggatgca gcagatctac ggagtgcggc gcgacaaaac ggcgcggtaa ttcaaatgag 3602
gaatattagc gagagttgaa atttcaacaa aatcagccgc atttttttca aacttaattgt 3662
atTTTTTTTc gTTTTTcTTt ttagtaatt cggcatttgg ggctagtgtg agcatttttaa 3722
agtaaaatcc tcattttccg aactccacct ttaaagggtg agtaccgaaa tttgagactt 3782
tgctTTTTtTt ggcccaaatt ggtccaaaac taccgaattt tgtaatgaga cgttctgaaa 3842
atttatccaa aaaatgttat ggcggttcaa agttcggcaa aatagggccc attttcagct 3902
aaaatcaaat tTTTTTTTc aactTTTTcG gtgtcgcaac gtctggagcc taatttttat 3962
ttattaatca cTTTTtaata aabattgtag cttttgatta ggcgtttatt cgtgatttta 4022
agtacattta tggTTTTtgg ggcacaaata aaagtttcat tttatgcccc aaaaaccata 4082
aatgtactta aatcagcgaa taaacgccta atcaaaggct acaatattta ttaaagagtg 4142
atgaataaat aaaaattagg ttccagacgt tgcgacaccg aaaaagttgg aaaaaatttt 4202
gatttttagct gaaaatgtgc cttattttgc cgcgaacttt gaaccgccat aacttttttt 4262
gagaaagaaa ttttcagaac gtctcattac gaaattcggg agttttaaac caatttgggt 4322
ctaaaaagtt tcaaatccca ataaaacata ccaaagtcct gtgaaattac aataaactat 4382
tcctaaacgt attataatcc attctcaatt cttgcag gaa gcg cat gta ttg gct 4437
                                Glu Ala His Val Leu Ala
                                210

cga atc gcc gag ctc cgt aag aac ggc tta tgg tcg aac agt cgt ctg 4485
Arg Ile Ala Glu Leu Arg Lys Asn Gly Leu Trp Ser Asn Ser Arg Leu
                                215                                220                                225

cca aag tgc gtc gaa cct gaa cgt aat aaa acg cat tgg gat tat cta 4533
Pro Lys Cys Val Glu Pro Glu Arg Asn Lys Thr His Trp Asp Tyr Leu
                                230                                235                                240

ctg gaa gag gtc aaa tgg atg gca gtt gat ttc cga acc gag acg aat 4581
Leu Glu Glu Val Lys Trp Met Ala Val Asp Phe Arg Thr Glu Thr Asn
                                245                                250                                255

acg aag cga aaa atc gcc aaa gtt ata gct cac gcc att gcg aaa cag 4629
Thr Lys Arg Lys Ile Ala Lys Val Ile Ala His Ala Ile Ala Lys Gln
                                260                                265                                270                                275

cac cgc gac aag cag atc gag att gag aga gcc gcc gaa cgg gag atc 4677
His Arg Asp Lys Gln Ile Glu Ile Glu Arg Ala Ala Glu Arg Glu Ile
                                280                                285                                290

aag gag aag cga aaa atg tgt gca gga atc gcg aag atg gta cgg gat 4725
Lys Glu Lys Arg Lys Met Cys Ala Gly Ile Ala Lys Met Val Arg Asp
                                295                                300                                305

ttc tgg tcg tct acg gat aaa gtt gtg gat att cga gcg aag gaa gtt 4773
Phe Trp Ser Ser Thr Asp Lys Val Val Asp Ile Arg Ala Lys Glu Val
                                310                                315                                320

ctg gag tcg agg ctc agg aag gcg aga aat aag cat ttg atg ttt gta 4821
Leu Glu Ser Arg Leu Arg Lys Ala Arg Asn Lys His Leu Met Phe Val
                                325                                330                                335

att gga caa gtc gat gaa atg agc aat att gtg caa gaa gga ctt gtt 4869
Ile Gly Gln Val Asp Glu Met Ser Asn Ile Val Gln Glu Gly Leu Val
                                340                                345                                350                                355

tca tcg tcg aaa tcc cca tca att gca tcg gat cga gat gat aaa gat 4917
Ser Ser Ser Lys Ser Pro Ser Ile Ala Ser Asp Arg Asp Asp Lys Asp
                                360                                365                                370

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FIGURE 19

gaa gaa ttc aaa gca cct ggc tct gat tca gaa tct gac gat gag cag	4965
Glu Glu Phe Lys Ala Pro Gly Ser Asp Ser Glu Ser Asp Asp Glu Gln	
375 380 385	
aca att gca aac gcg gaa aag tca cag aaa aag gaa gat gtt cga cag	5013
Thr Ile Ala Asn Ala Glu Lys Ser Gln Lys Lys Glu Asp Val Arg Gln	
390 395 400	
gaa gtt gat gct ctt caa aac gag gca act gtg gat atg gat gac ttt	5061
Glu Val Asp Ala Leu Gln Asn Glu Ala Thr Val Asp Met Asp Asp Phe	
405 410 415	
ttg tac act tta ccg ccg gaa tat ctg aag gct tat ggt ctg acg cag	5109
Leu Tyr Thr Leu Pro Pro Glu Tyr Leu Lys Ala Tyr Gly Leu Thr Gln	
420 425 430 435	
gag gat ttg gag gag atg aag cgc gag aaa ttg gag gag cag aag gct	5157
Glu Asp Leu Glu Glu Met Lys Arg Glu Lys Leu Glu Glu Gln Lys Ala	
440 445 450	
cgg aag gaa gct tgt ggt gat aat gag gag aaa atg gag att gat gaa	5205
Arg Lys Glu Ala Cys Gly Asp Asn Glu Glu Lys Met Glu Ile Asp Glu	
455 460 465	
gttcgtagga tgctcctaaa aaaattacct aaaaaaaatc gattttccct ggaaaaaatc	5265
ctctggaaat gacccgaaac gtcattggcg ctcgaaatct tgaaaaaaa aaccccccaa	5325
atttccagct aaaatctcaa attttattgc atatttttgt agttcttttg ttgtccgagg	5385
tgcgtttttc agctgaaaat gtacctgaat ctgcaagtaa acgaccaata tatgcaataa	5445
atgatgataa ttaatttccg atactgaaat gtgggcgaaa tttagattt cgactgaaaa	5505
cgtcttaaaa atcacccaaa acccggttt accgcacgaa ggtttgaaga aaatggccaa	5565
tttttagcca aaatctcaaa tttcgtccac ttttcagtca gaaattagtt ttttgaaatt	5625
aattaacacc ttttattgca tattttcgtc gtttattcgt tgatcgagggt gctttttcgg	5685
tcgatgggtg cacaaattcg gtaattgtgc atccatcggc tgaaaatgct ccagaatttg	5745
cgaatgaacg gtgaaaattt aagatttttag attgaaataa gccgtttttt agagaaaatt	5805
ggtcgttttg agacattaaa ttcaatttaa atcccctctt tattttcag agc cca tca	5863
Ser Pro Ser	470
tca gat gct caa aag cct tcc acc tca agc tca gat ctc acc gcc gag	5911
Ser Asp Ala Gln Lys Pro Ser Thr Ser Ser Ser Asp Leu Thr Ala Glu	
475 480 485	
cag ctt caa gat cca aca gct gaa gac ggc aac ggt gat ggt cat ggt	5959
Gln Leu Gln Asp Pro Thr Ala Glu Asp Gly Asn Gly Asp Gly His Gly	
490 495 500	
gta ctt gaa aac gtg gat tac gtg aag ctc aac agt cag gat agt gat	6007
Val Leu Glu Asn Val Asp Tyr Val Lys Leu Asn Ser Gln Asp Ser Asp	
505 510 515	
gaa cga caa caa gag ttg gcg aat atc gca gaa gaa gcg ctg aaa ttc	6055
Glu Arg Gln Gln Glu Leu Ala Asn Ile Ala Glu Glu Ala Leu Lys Phe	
520 525 530	
cag cca aaa gga tat aca ctt gag acg aca caa gtc aag acg ccc gta	6103
Gln Pro Lys Gly Tyr Thr Leu Glu Thr Thr Gln Val Lys Thr Pro Val	

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FIGURE 19

535	540	545	550	
cca ttc ctg att cga gga caa ctg aga gaa tat caa atg gtt gga ttg				6151
Pro Phe Leu Ile Arg Gly Gln Leu Arg Glu Tyr Gln Met Val Gly Leu				
	555	560	565	
gat tgg atg gtt aca ctt tat gag aag aat ttg aat gga att ctt gcc				6199
Asp Trp Met Val Thr Leu Tyr Glu Lys Asn Leu Asn Gly Ile Leu Ala				
	570	575	580	
gac gag atg ggc ctg gga aag acg att caa acg att tcc ctg ctg gct				6247
Asp Glu Met Gly Leu Gly Lys Thr Ile Gln Thr Ile Ser Leu Leu Ala				
	585	590	595	
cat atg gct tgt agt gaa tgc att tgg gga cca cac ttg att gtt gtg				6295
His Met Ala Cys Ser Glu Ser Ile Trp Gly Pro His Leu Ile Val Val				
	600	605	610	
ccg acg tct gtc att ctg aat tgg gag atg gag ttc aag aaa tgg tgt				6343
Pro Thr Ser Val Ile Leu Asn Trp Glu Met Glu Phe Lys Lys Trp Cys				
	615	620	625	630
ccg gct ctg aag att ttg acg tat ttt ggt acg gcg aag gag cgt gcc				6391
Pro Ala Leu Lys Ile Leu Thr Tyr Phe Gly Thr Ala Lys Glu Arg Ala				
	635	640	645	
gag aag cgg aag gga tgg atg aag ccg aat tgt ttc cat gtg tgc atc				6439
Glu Lys Arg Lys Gly Trp Met Lys Pro Asn Cys Phe His Val Cys Ile				
	650	655	660	
aca tca tac aag acg gtt act caa gat att aga gct ttt aag cag agg				6487
Thr Ser Tyr Lys Thr Val Thr Gln Asp Ile Arg Ala Phe Lys Gln Arg				
	665	670	675	
gtgcgtagaa attttgaaga tttgcggcga atttggcgaa tttgcataat ttttttaaaa				6547
ccaatttttac cgataattgc gaaatttttc aatttttatac agtggtcgga aattgctata				6607
attagtataa tttttgcaaa aattggtact tttttcgaaa ttttgaacca ccataaaaca				6667
tttttgaaca atttttaaga ggtttaataa cgaaattcgt tcatttgaac acattttggc				6727
gatatgaatc gcccgaataa gtccccaat agacctaat tcttaacaaa aattttaaaaa				6787
aaaaatggccc aaaattgtct caaaatttcg aaaaaaaaaac cgtaatttca gctgaaatct				6847
caaaatttgc caaattttcc gtctcacgga gatcagaaaa agttttttgc atttttttgt				6907
ggtttatttt agcgttattt cgtaatttta gatacatttt agcccaattt ttgcaaaaaat				6967
tatactaatt atagcaattt ctgacccctg acaaactttg aaattatcgg taaacttggt				7027
ataaatgggt tttttccaaa tttttaaaagc gatattaaag gtggagtacc acaatttgag				7087
gctttgtttt tttttttgga cccaaattgg tccaaaaacta ccgaatttcg taatgagacg				7147
ctctgaaaat ttctttctca aaaaaaaagt tacggcggtt caaagttcgc ggcaaaaataa				7207
ggcccathtt cagctaaaaa caaaattttt tcccaacttc tcggtgtctc aacgcctgga				7267
acctaatttt tatatttca tcaactttta ataaatattg tggcttttga ttgggctttt				7327
attcgttgat ttaagtacat ttatggtcag tggggcacaa aatgtaactt tttttcccaa				7387
agaccataaa tgtactttta tcaacgaata aacgcccatt caaagaccac aatattttatt				7447
taaaagtaat gaataaataa taattaggtt ccagacgttg cgacaccgag aagttgga				7507
atttttttat tttagctgaa taagggcctt attgtctcaa actttgaacc gccataactt				7567
ttttttgaga acgtctcgtt acgaaattcg gtagttttgg accaatttgg gtctaaaaaa				7627
acaaagtctc aaatttcttg ttagagattt tttaaaaatt gatatttttt ttttcag gcc				7687
				Ala

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FIGURE 19

tgg cag tac cta att ctc gat gaa gct caa aat atc aaa aac tgg aag	7735
Trp Gln Tyr Leu Ile Leu Asp Glu Ala Gln Asn Ile Lys Asn Trp Lys	
680 685 690 695	
tcc caa cgt tgg cag gct ctt ctg aat gtc cgt gct cga cgt cgc ctt	7783
Ser Gln Arg Trp Gln Ala Leu Leu Asn Val Arg Ala Arg Arg Leu	
700 705 710	
ctc ctg acc gga act cca ctt cag aac tct cta atg gaa ctg tgg tcg	7831
Leu Leu Thr Gly Thr Pro Leu Gln Asn Ser Leu Met Glu Leu Trp Ser	
715 720 725	
ttg atg cat ttt ttg atg cca aca ata ttc tca agt cat gat gat ttc	7879
Leu Met His Phe Leu Met Pro Thr Ile Phe Ser Ser His Asp Asp Phe	
730 735 740	
aag gat tgg ttc tcg aat ccg ttg aca ggg atg atg gaa gga aat atg	7927
Lys Asp Trp Phe Ser Asn Pro Leu Thr Gly Met Met Glu Gly Asn Met	
745 750 755	
gaa ttc aat gct cca cta atc gga cga ctt cac aaa gtg ctc cgt ccg	7975
Glu Phe Asn Ala Pro Leu Ile Gly Arg Leu His Lys Val Leu Arg Pro	
760 765 770 775	
ttt att ctg cgg cgg ctc aag aag gaa gtt gag aag cag ctg cca gag	8023
Phe Ile Leu Arg Arg Leu Lys Lys Glu Val Glu Lys Gln Leu Pro Glu	
780 785 790	
aag act gag cat att gtg aat tgt tcg ttg tca aag cgg cag aga tac	8071
Lys Thr Glu His Ile Val Asn Cys Ser Leu Ser Lys Arg Gln Arg Tyr	
795 800 805	
ctg tac gat gac ttt atg agt cgt aga tca aca aag gag aat cta aag	8119
Leu Tyr Asp Asp Phe Met Ser Arg Arg Ser Thr Lys Glu Asn Leu Lys	
810 815 820	
tct gga aat atg atg tcg gtg ctc aac att gtg atg caa ctc cga aaa	8167
Ser Gly Asn Met Met Ser Val Leu Asn Ile Val Met Gln Leu Arg Lys	
825 830 835	
tgt tgt aat cat ccg aat ctc ttc gag ccg cgg cca gtt gtt gct ccg	8215
Cys Cys Asn His Pro Asn Leu Phe Glu Pro Arg Pro Val Val Ala Pro	
840 845 850 855	
ttc gtc gtt gag aag ctt cag ctc gat gtt ccg gct cgt ctc ttt gaa	8263
Phe Val Val Glu Lys Leu Gln Leu Asp Val Pro Ala Arg Leu Phe Glu	
860 865 870	
att tcg cag caa gat ccc tcc tcc tcc tca gct agt caa att ccg gaa	8311
Ile Ser Gln Gln Asp Pro Ser Ser Ser Ser Ala Ser Gln Ile Pro Glu	
875 880 885	
att ttc aat tta tcc aaa atc ggc tat caa tct tcc gtt cga tct gca	8359
Ile Phe Asn Leu Ser Lys Ile Gly Tyr Gln Ser Ser Val Arg Ser Ala	
890 895 900	
aaa cca ctc atc gaa gag ctt gaa gca atg agc act tat ccg gag cca	8407

FIGURE 19

Lys Pro Leu Ile Glu Glu Leu Glu Ala Met Ser Thr Tyr Pro Glu Pro
 905 915
 cga gca cca gaa gtt ggc gga ttt cgg ttc aat cgg acg gct ttt gtt 8455
 Arg Ala Pro Glu Val Gly Gly Phe Arg Phe Asn Arg Thr Ala Phe Val
 920 925 930 935
 gca aag aat ccg cat acg gaa gag tcg gag gac gaa ggt gtt atg aga 8503
 Ala Lys Asn Pro His Thr Glu Glu Ser Glu Asp Glu Gly Val Met Arg
 940 945 950
 agt cgt gtt ctg gtgaattttt aggaaaattg agaaaatgat ctaattgttg 8555
 Ser Arg Val Leu
 955
 aatttttttaa agaatttatg ggccacaagc cgatttgccg gaaattttga tttttggcga 8615
 tttgccgaaa-attttgattt ttggcgattt-gccagaaatt-ttgatttttg gcaatttatcc 8675
 gatttgccgg aaattttgat ttttggcgat ttgccagaaa ttttgatttt tggcaattat 8735
 ccgatttgcc ggaaattttg aattttggca attttccgat ttgccggaaa ttttgatttt 8795
 tggcaatttg ccgaattgcc ggaaattttg atttttggca atttgccgaa ttgccggaaa 8855
 ttttgatttt tggggatttg ccggaaattt tgatttttgg caatttgcct atttgtcgga 8915
 aattttgatt tttggcaatt tgccgatttg tcggaaattt tgatttttgg caatttgcg 8975
 atttgccgga aattttgatt tttggcaatt ttccgatttg ccaaaaattt tgatttttgg 9035
 cgatttgccg atttgccgga aaaacatttt gtgagccaat tttctcgaaa tttgggcttc 9095
 aatattttca aattattcca aattttccac tgattccgaa tatctaagta aaaaaaatt 9155
 ccctgatttt atatttcagc ttaaaatcgc taattttcgc gtcagagacg acgtcatgtg 9215
 tcgatttact ggatttttaa tctttgtcgg atgctaattt ccgtttttca acgagtttcc 9275
 ttcatttcca tcggtttttg acgaagtttt ctttgaaaat atgttcttaa ggtcaattaa 9335
 acgtttttatt atcaaaaaaa actagcaaaa ttggctttta aaacacattt tcacagaaaa 9395
 ctccgacaaa aaccgacgaa aatgaaggaa acccccgtt tgaaaacaga aattagcatc 9455
 tgataaagat taaaatcccg taaatcgaca catggcgtct ggcgtctctg gcacgaaaag 9515
 tcgcgatttt aagctgacat acaaaaaaag agggatatat ttttttacga atttttcaca 9575
 tagatattcg aaatcagggg ggaaaatttg gagaaatttg agaaaatttc tcagatttgcg 9635
 gattaataat attcaatttt tgttttctta tattaaaaa aaattaactt ttataatttt 9695
 tcag cca aaa cca att aat gga aca gct caa cca ctt caa aat gga aat 9744
 Pro Lys Pro Ile Asn Gly Thr Ala Gln Pro Leu Gln Asn Gly Asn
 960 965 970
 tca ata cca caa aat gct cca aat cgt cca caa act tca tgc att cgt 9792
 Ser Ile Pro Gln Asn Ala Pro Asn Arg Pro Gln Thr Ser Cys Ile Arg
 975 980 985
 tca aaa acc gtc gta aat aca gtt cca ctg acc atc tcc acc gat cga 9840
 Ser Lys Thr Val Val Asn Thr Val Pro Leu Thr Ile Ser Thr Asp Arg
 990 995 1000
 agt ggt ttt cat ttt aat atg gcc aat gtt gga aga ggt gtt gtt cgt 9888
 Ser Gly Phe His Phe Asn Met Ala Asn Val Gly Arg Gly Val Val Arg
 1005 1010 1015
 ttg gat gat tca gca cgt atg agc cca ccg ctc aaa cgt cag aag ctc 9936
 Leu Asp Asp Ser Ala Arg Met Ser Pro Pro Leu Lys Arg Gln Lys Leu
 1020 1025 1030
 acc gga act gca acg aat tgg agt gat tat gtt ccg cga cac gtt gtt 9984
 Thr Gly Thr Ala Thr Asn Trp Ser Asp Tyr Val Pro Arg His Val Val
 1035 1040 1045 1050

Title: RB PATHWAY AND CHROMATIN REMODELING
 GENES THAT ANTAGONIZE LET-60 RAS SIGNALING
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FIGURE 19

gaa aag atg gaa gaa tcg aga aaa aac cag ctg gaa att gtt cga agg 10032
 Glu Lys Met Glu Glu Ser Arg Lys Asn Gln Leu Glu Ile Val Arg Arg
 1055 1060 1065

cga ttt gag atg att cgt gct ccg att att cca ctg gaa atg gtt gcg 10080
 Arg Phe Glu Met Ile Arg Ala Pro Ile Ile Pro Leu Glu Met Val Ala
 1070 1075 1080

ctg gtt cga gag gaa att att gca gaa ttt cca cgt ttg gct gtg gaa 10128
 Leu Val Arg Glu Glu Ile Ile Ala Glu Phe Pro Arg Leu Ala Val Glu
 1085 1090 1095

gag gac gag gtt gtg cag gag agg ctt ttg gag tat tgc gag ttg ttg 10176
 Glu Asp Glu Val Val Gln Glu Arg Leu Leu Glu Tyr Cys Glu Leu Leu
 1100 1105 1110

gtg caa aggtagaatt ttgaaaatta ttacttttgct tttttttaaa ccaaaattgg 10232
 Val Gln
 1115

ccccaaacta ccgaatttcg taatgagaca ttctgaaagc ttctcaaaaa aaaagttttg 10292
 gccgctcaaa gttcgggaaa ataaggccca ttttcagctg aaatcaaaat tttttccaac 10352
 ttctcgggtg cgcaacgtct ggaactaaaa ttttgaaaa cgagaaattt tccatttttt 10412
 gcaagctgaa aaatcaaagt ttttttttcc tcaaaattgg acaaacaaaa aaattttttt 10472
 ttgaaaattg atcgaaaaaa ttcaaaattt ctataatttt tcgatttttt aaataaaact 10532
 ttcatcattt ttcttccaaa tttagttttc tcgattttta cttttttcaa aaaaaaattt 10592
 tttatacga aaaaaattca attttagctc taattctttt ttagacccaa attggtccaa 10652
 aactaccgaa tttcgtaatg agacgttctg aacattttct aaaaaaaagt tatgacgggt 10712
 caaagtccg caaaataagg cccattttca tataaaatca aatttttttt ctaacttctc 10772
 ggtgtcacaa cgtctggaac ttaattttta ttttaattatt acttttcaat aaatattgtg 10832
 gtcttttatt aggcgtttat ttgttgattt aagtacattt atgggtcaagt ggggccccaa 10892
 taaaagttaac attttgtgcc cacatgacca taaatgtact taaatcaacg aataaacgcc 10952
 taatcaaaagg ccacaatatt tattaataag tgttgaataa ataaaaatta ggtccagac 11012
 attgtgacac cgagaagtta aaaaaaattt tgatttttagc tgaaaatggg ccttattttg 11072
 ctgaacttta aaccgctata actttttttt gagaaatttt cagaacgtct cattacgaaa 11132
 ttcggtagtt ttggaccaat ttgggtctaa aaaagaatta gagctaaaat tgaattttct 11192
 tcgtattaaa aatttttttt ttgaaaaaag taaaaatcga gaaaactaaa tttggaagaa 11252
 aaatgatgaa aatttttatt aaaaaatcga aaaatttatag aaattttgat cgattttttc 11312
 gatcaatttt caataaaaaa ttttttgttt gtccaatttt gaggaaaaaa aaaactttga 11372
 tttttcagct tacaaaaaat ggaaagtttc tcgttttcca attttttgat gtggattttt 11432
 atgagaaaaa atatataatg tcacaaaaaa tagattatta tctaaaaatc gaaaaaatta 11492
 aattttccag ttttcaggaa aaaaatcggt aagaaattgt ttttccatta aagggtggagt 11552
 accgaatttt gagacgtgc ttttttagac ccaaaatggt ccaaaactac cgaatttcgt 11612
 aatgatacgc tctgaaaaat tttcaaaaaa aaagtgtgga ccgctcaaag ttttgaaaaa 11672
 atggcatatt tttagctaaa atctcaaatt ttggcaactt atcggtgtcg cagcggttgg 11732
 aacttaattt ttatttaatt gtcattcatt aatgcatggt ttggcatttc attatgtgtt 11792
 atttcgttga ttgagatgct ttttgtgcct gcacgacca aaaaaccatc tcaatcaacg 11852
 aaataacaca taataaaatg ccaaaatgat cattaaagga tgataatcaa ataaaaatta 11912
 agtttcaacc gctgcgacac cgctaagttg ccaaaatttg agatttttagc taaaaatggt 11972
 ccattttttt aaaactttga gcggtcacia cttttttttt gagaaatttt cagagcgtct 12032
 cattacgaga attggtaggt tcggaccaat ttgggtctaa aaaagcagcg tctcaaaatt 12092
 cgttacttca cttttaaagt tttcaattta aagtataaat tatccaatca aaaattgacg 12152
 aaaaaatttt ttaaaaattt tttcttcga aaaaaaattt aattttaatt tttgtt aga 12211
 Arg

FIGURE 19

ttc gga atg tac gtc gaa cca gtg ctg acc gat gct tgg cag tgt cgt	12259
Phe Gly Met Tyr Val Glu Pro Val Leu Thr Asp Ala Trp Gln Cys Arg	
1120 1125 1130	
cca tca tcg tct ggt ctt cca tca tat att cgc aac aat tta tca aat	12307
Pro Ser Ser Ser Gly Leu Pro Ser Tyr Ile Arg Asn Asn Leu Ser Asn	
1135 1140 1145	
atc gag ctg aat tct cgt tct ctt ctc ctc aac acc tcc act aat ttc	12355
Ile Glu Leu Asn Ser Arg Ser Leu Leu Leu Asn Thr Ser Thr Asn Phe	
1150 1155 1160 1165	
gat acc cga atg tcg atc tca cgt gct ctt caa ttc cca gaa ctc cgt	12403
Asp Thr Arg Met Ser Ile Ser Arg Ala Leu Gln Phe Pro Glu Leu Arg	
1170 1175 1180	
ctg atc gag tac gat tgt gga aag ctt cag acg ttg gct gtt ctg ctt	12451
Leu Ile Glu Tyr Asp Cys Gly Lys Leu Gln Thr Leu Ala Val Leu Leu	
1185 1190 1195	
cgt cag ttg tac ctg tac aag cac aga tgt ctg atc ttc acg caa atg	12499
Arg Gln Leu Tyr Leu Tyr Lys His Arg Cys Leu Ile Phe Thr Gln Met	
1200 1205 1210	
tca aag atg ctc gac gtt ctg cag acc ttc ctt tct cat cac ggt tat	12547
Ser Lys Met Leu Asp Val Leu Gln Thr Phe Leu Ser His His Gly Tyr	
1215 1220 1225	
cag tat ttc cgc ctc gac ggt acc act ggt gtc gaa caa aga cag gcg	12595
Gln Tyr Phe Arg Leu Asp Gly Thr Thr Gly Val Glu Gln Arg Gln Ala	
1230 1235 1240 1245	
atg atg gag cgg ttc aac gcg gat ccc aag gtg ttt tgc ttc att ctg	12643
Met Met Glu Arg Phe Asn Ala Asp Pro Lys Val Phe Cys Phe Ile Leu	
1250 1255 1260	
tcg acg aga tcc ggt ggt gtt gga gtc aat cta acc ggt gct gac act	12691
Ser Thr Arg Ser Gly Gly Val Gly Val Asn Leu Thr Gly Ala Asp Thr	
1265 1270 1275	
gtg atc ttc tac gat tcg gat tgg aat ccg acg atg gat gct cag gct	12739
Val Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Met Asp Ala Gln Ala	
1280 1285 1290	
cag gat aga tgt cat cgt atc gga cag acg agg aat gtc tcg att tat	12787
Gln Asp Arg Cys His Arg Ile Gly Gln Thr Arg Asn Val Ser Ile Tyr	
1295 1300 1305	
cga ttg att tcc gag cga aca att gag gag aat att ctg aga aag gca	12835
Arg Leu Ile Ser Glu Arg Thr Ile Glu Glu Asn Ile Leu Arg Lys Ala	
1310 1315 1320 1325	
aca cag aag cgg cga ctt gga gag ttg gca att gac gag gct ggc ttc	12883
Thr Gln Lys Arg Arg Leu Gly Glu Leu Ala Ile Asp Glu Ala Gly Phe	
1330 1335 1340	
aca ccc gag ttc ttc aaa caa tct gac agt att cgg gat ctt ttt aat	12931

FIGURE 19

Thr Pro Glu Phe Phe Lys Gln Ser Asp Ser Ile Arg Asp Leu Phe Asp
1345 1350 1355

gga gag aat gtg gaa gtg act gct gtg gca gat gtt gcg acg acg atg 12979
Gly Glu Asn Val Glu Val Thr Ala Val Ala Asp Val Ala Thr Thr Met
1360 1365 1370

agc gag aaa gaa atg gag gtt gcg atg gca aag tgt gaa gat gaa gct 13027
Ser Glu Lys Glu Met Glu Val Ala Met Ala Lys Cys Glu Asp Glu Ala
1375 1380 1385

gat gtg aat gcg gcg aag att gcg gtg gcc gag gcg aac gtt gat aat 13075
Asp Val Asn Ala Ala Lys Ile Ala Val Ala Glu Ala Asn Val Asp Asn
1390 1395 1400 1405

gcg gag ttt gat gag aaa tca ttg ccg ccg atg agc aat ttg caa gga 13123
Ala Glu Phe Asp Glu Lys Ser Leu Pro Pro Met Ser Asn Leu Gln Gly
1410 1415 1420

gat gag gag gct gat gag aag tat atg gag ttg ata caa c aggtaaaatt 13173
Asp Glu Glu Ala Asp Glu Lys Tyr Met Glu Leu Ile Gln
1425 1430

cgccggaat cggaatttt cccatttaga atatcaaatt ttgcccgatt gtgtcgtttt 13233
ttgatttttc gatttattcg atttgttttt gagggaaaat cggaataatg ttcagaaaat 13293
taaccataac atgtgatctt tttaaaatct tagcgcaaat gtcttctaaa aaataaagaa 13353
tgacaaaaaa ttttaagcta atttttgaaa aaccaaagaa aaaatttaga tttttcgatg 13413
ttttccgaga caaaaagaca aaaacggaaa ttgtcgaaaa tgaatgaaat ttttaatttt 13473
tcagcaaaaa aaaaatagta cttaatttta aaaaatgtga tcatttcggt aggaaaatct 13533
ggaaaaatcg attttcaaac aaaaaaaac cgagcctcta caatcttttt ttttcccgaa 13593
atctccagaa cttctcacia taacaactat ataaatttca aaatttc ag ctc aaa 13648
Gln Leu Lys
1435

cca atc gaa cga tat gcc att aac ttt ctt gag aca cag tac aag cca 13696
Pro Ile Glu Arg Tyr Ala Ile Asn Phe Leu Glu Thr Gln Tyr Lys Pro
1440 1445 1450

gaa ttt gag gaa gaa tgc aaa gag gca g aggtatatta ttccattcat 13744
Glu Phe Glu Glu Glu Cys Lys Glu Ala
1455 1460

ctgacttttt tttttttttt ttaaatttaa atttcaccaa attaatatc ag gct ctt 13801
Glu Ala Leu
1465

atc gac caa aaa cgc gaa gaa tgg gac aaa aat ctc aac gat acc gcc 13849
Ile Asp Gln Lys Arg Glu Glu Trp Asp Lys Asn Leu Asn Asp Thr Ala
1470 1475 1480

gtc att gac ctc gac gat tcg gat agt ctg ctg ctc aac gat cct tcg 13897
Val Ile Asp Leu Asp Asp Ser Asp Ser Leu Leu Leu Asn Asp Pro Ser
1485 1490 1495

act tct gcc gat ttt tat cag agc tca agt ctt tta gac g aggtacgcga 13947
Thr Ser Ala Asp Phe Tyr Gln Ser Ser Ser Leu Leu Asp
1500 1505 1510

FIGURE 19

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tcgtcgtcgt cgcagcagca gccttctcca aaaagccgct caaaaaccgg caaaaaagcc 14007
tcaaaacttc caaatctcgt ctcgctcccc gtctaagcgt aaatctcagg ctcccttccct 14067
cgatccatat gtttcgtacg caccgcacgc gctcgcttct cccccggatt ccccgcgtaa 14127
gagaagatca cgtggtgccc gtagtttagg tagtggtggt ggtggtggtg gtggtagtag 14187
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ggattattgc caagaagagg aagtgaagcg aaatccggca gaaaagggtc cggcgaaaag 14307
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gctgatttcg ttgcaaaaag ctgtgccagt tgtacctcgg cccaacaac aagcaccacc 14487
acagctcatc aaaaagcacc agcagactct gatgctgtg aagggtgctc agattagtg 14547
tggtggtggt ggtactccag gaccatccag tgtatcgcca ggtccatcaa tctccgaag 14607
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tccaacagct cctgcagcag ctccacgcca gttcgtcgt ccgctcgtcga gaggtcgagt 14787
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acctccagat cgcccaggat ttggaatcta tgagaagccg agattctcac ttggatcacg 14967
aagaagccgt ggagattcgg gcccggaaga tccggcgcca ccacagccac caccaccacc 15027
cacttctagg ccaccgccac aagcctaggc gctaggattt tctttttttt ttgttgatt 15087
tttgccttt tttgtctct tcatgatttt ataactcat tttgctttaa tatttccatt 15147
tttttgatg tgtggaattt ttttttttga aaatcgggaa aaaacgaaaa atttgaactt 15207
tttggtgatt ttcagagaaa aatccgtttt taaatgaaaa aatcggaata attcagattt 15267
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aaaaaagtaa attttcagaa ttatcagcca agtttttgcg attttttgaa aaatttcaat 15387
ttttggcaat ttttgggaaa aaatcaattt ttaattcaga aaattggaaa aattaagatt 15447
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cggaattttt ttaatttttc gaataaaaaa aatcgaagaa attccaaaac ttgcgtttt 15567
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aaatttttgt gatttttcga tttttttcac tccaaaaaaa ttccacacag caaaaaataa 15867
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aagtttttaa cactgatttt ctggtttttt tttttttttg cagaattttt cagagatagg 16227
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ttaattttgg ctttagagat tcgatcgaaa aaattgcgaa agtggcgaga aatctcactg 16407
gtttgatgtt tgacccctca ctatagaaaa tttgaaaaaa aaaaaaaaaa aaaaaaacta 16467
gacgaaattt gtggaaatct tgctggagtt tgacgagtcg atggtggatt tttcttgaaa 16527
cgaatgaaac ggtgattttg gatcggagaa atatggcgaa aaatggtgag aaatgacgag 16587
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gcacaataaa tttttgctga aacaagtgcg cgcctttgaa gagtactgca atttcaaaca 17187
cggttttttg gttggaaagc acagtacttt tcaaaagggtg cacaccttct cgaatttctc 17247
ttcgtgtcga gaccaagaat gccatttttc gattttttaa aaatcaaaaa aaaaattacc 17307

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Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE LET-60 RAS SIGNALING

Applicant(s): Horvitz *et al.*

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Glu Ile Lys Phe Tyr Asp Glu Leu Asp Asp Ile Met Pro Ile
1515 1520

tg	g	ctt	cca	cca	tca	cca	cca	gat	tcg	gat	gcg	gat	ttc	gac	ttg	aga	18965
Trp	Leu	Pro	Pro	Ser	Pro	Pro	Asp	Ser	Asp	Ala	Asp	Phe	Asp	Leu	Arg		
1525					1530					1535					1540		

atg gaa gat gat tgt ctc gat ctg atg tat gaa att gaa caa atg aac 19013
Met Glu Asp Asp Cys Leu Asp Leu Met Tyr Glu Ile Glu Gln Met Asn
1545 1550 1555

gag gct cgc cta cca caa gtt tgt .cat gaa atg aga cgt ccg ttg gct 19061
Glu Ala Arg Leu Pro Gln Val Cys His Glu Met Arg Arg Pro Leu Ala
1560 1565 1570

gaa aaa cag cag aaa cag aac acg ttg aat gcg ttt aa tggtaatatt 19109
Glu Lys Gln Gln Lys Gln Asn Thr Leu Asn Ala Phe Lys
1575 1580 1585

tcaaaaaaaa	aatttttttg	aaaaaattca	attaaattcg	attttgagca	atttttatcg	19169
tgaagattgc	ataattttga	gattttgcgc	caagattttt	gttaaattga	aaaaaagaga	19229
tgtgcgcctt	tatggagtac	tgtagttttg	aaaattgaaa	ttacagtact	ctgtttaaag	19289
gcgcacacat	gtattacgta	gcgaaaagaa	aagtacagta	attagttaaa	taagactact	19349
gtagcgcttg	tgtcgattta	cgggctctga	attttatatg	aatttttgaa	aactagaaac	19409
atctcaaatt	gcataaaatt	accatttgaa	cctcccgcca	agtgattttg	ttcgacgggg	19469
cgcgcttgca	cgttttctat	tttaatttaa	ttcaattttt	tttgcttaac	tctcaccgat	19529
ttttctatgt	ttcagtttga	ttttgatgga	aattttggaga	caatatcaac	ataaatgctt	19589
ttcaatcgaa	aatgtgcatt	tatatggaca	ttttctccga	atttccatca	aaattaaact	19649
gaaaacacga	aaaatcggtg	agaattaaag	gaaaaaattg	agttaaatga	aaatagaaaa	19709
cgtqcaagcg	cgctccatcg	aacaaaatca	attggcggga	ggttcaaatg	ggaattgtat	19769

FIGURE 19

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gcaatttttca aaaggtcgta taaaattttg aagaaagcaa attaaattta aaaaatcgag 19829
ctcgtaaaatc gacacaggcg ctaatttttca aaaaaataaa atgacaccca aaaaatcata 19889
agaaaatcat aaataaatat tacgggaaca caaaactcag agaaccgta ttgcacaaca 19949
tatttgacgc gcaaaatatg aaatatctcg tagcgaaaag aaaactaccg taatttaaaa 20009
acattttaat gactactgta gcgcttgtgt cgatttacga gatctcgatt ttctaaataa 20069
atttttttaa aaatgatgtc agcgatattc catttgactt tgtttcttcg tattttttc 20129
tcatttttgc ttgattttat ttaattttat aattttattt aaaatcaagc aaaaacgaga 20189
aaataatacg aagaaacgga gttaaattga atatcgctga cataatttaa aaaaaaatt 20249
taattagaaa atcgagatcc cgtaaatacg cacaagtagt catagtacag tagtcattta 20309
actaattact gtacttttct ttctcgctgc agatatttca tatttttatt catattttta 20369
tttattttca tatttttata tatatatata tatatatatt tcttggcggt ctaatgcagt 20429
ttctctcaat taattcc a gac att cta tcg gca aaa gaa aag gaa tcg gtg 20480
          Asp Ile Leu Ser Ala Lys Glu Lys Glu Ser Val
                        1590                        1595

tac gat gcg gtc aac aag tgc ctt caa atg cca caa tcc gaa gcg atc 20528
Tyr Asp Ala Val Asn Lys Cys Leu Gln Met Pro Gln Ser Glu Ala Ile
          1600                        1605                        1610

aca gca gaa tct gca gcg tct cca gca tac acg gaa cac tca tca ttc 20576
Thr Ala Glu Ser Ala Ala Ser Pro Ala Tyr Thr Glu His Ser Ser Phe
          1615                        1620                        1625

tcg atg gat gat aca agc cag gat gcg aag att gag cca agt ttg act 20624
Ser Met Asp Asp Thr Ser Gln Asp Ala Lys Ile Glu Pro Ser Leu Thr
          1630                        1635                        1640

gaa aat caa caa ccc acc acc acc gcc act act act act aca gta ccc 20672
Glu Asn Gln Gln Pro Thr Thr Thr Ala Thr Thr Thr Thr Thr Val Pro
          1645                        1650                        1655                        1660

caa caa caa caa caa cag cag cag caa aaa tcg tcg aaa aag aag aga 20720
Gln Gln Gln Gln Gln Gln Gln Gln Gln Lys Ser Ser Lys Lys Lys Arg
          1665                        1670                        1675

aat gat aat cga a cggtacggag gttactagcg aacaatttca agaaattttg 20773
Asn Asp Asn Arg
          1680

aatttgtgaa aattcaattc cggcaatttt tcgatttgcc ggaactttta attttcgccg 20833
aattgtcaat ttgccgaaa ttttgatttc cgccgaattg tcgatttgcc ggaacttttc 20893
attttcggca aattttcgat ttgccggaac ttttaatttt tgacaaattg tcgatgtgcc 20953
ggaaattttg attttcgaca atttgctgat ttgccgaaa tttcaatccc aacaattttc 21013
cgatttgccg gaaattttcaa tcccaacaat tttccgattt gccggaaatt tcaatcccaa 21073
caattttccg atttgccgga aatttcaatc ccaacaattt tccgatttgc cggaaatttc 21133
aatcccagca attttccgat ttgccgaaa tttcaatttc ggcaattttt cgatttgccg 21193
gaacttttca ttttcggcaa agtgtcgatt tgccggaact tttcattttc gccgaattgt 21253
cgatttgccc gaacttttaa tttttgacaa attgtcgatt tgctggaaat tttgattttc 21313
gacaatttgc caatttgccg gaacttttaa tttttgacaa attgtcgatt tgccggaaat 21373
tttgattttc gacaatttgc caatttgccg gaacttttca tttttgcaa attgtcgatt 21433
tgccggaaat ttttaattccg gcaattttgc gatttgccgg aaatttcaat tccggcaatt 21493
taaaaacact aaaaaccaa aattttcggt tttcccggtt ttcgatgtt cagcttttct 21553
caaaaattg cgattccccg aaaaatcgaa acaatttttc ggggttaaaac cgggaaattc 21613
ctaaattcct atttaaaaga attgaaaaaa aactctcaaa attcc ag gct caa aat 21669
                                Lys Ala Gln Asn

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FIGURE 19

cga aca gct gaa aat ggt gtg aaa cga gcg aca act cca cca cca tca	21717
Arg Thr Ala Glu Asn Gly Val Lys Arg Ala Thr Thr Pro Pro Pro Ser	
1685 1690 1695 1700	
tgg cgt gaa gag cca gat tat gat gga gcc gaa tgg aat ata gtt gaa	21765
Trp Arg Glu Glu Pro Asp Tyr Asp Gly Ala Glu Trp Asn Ile Val Glu	
1705 1710 1715	
gat tat gca cta ctt caa gca gtt caa gtc gaa ttt gca aat gct cat	21813
Asp Tyr Ala Leu Leu Gln Ala Val Gln Val Glu Phe Ala Asn Ala His	
1720 1725 1730	
tta gtc gaa aaa tcg gcg aat gag gga atg gtg ttg aac tgg gaa ttc	21861
Leu Val Glu Lys Ser Ala Asn Glu Gly Met Val Leu Asn Trp Glu Phe	
1735 1740 1745	
gtg tcg aat gcc gtt aat aag cag aca aga ttt ttc cgc tcg gcc cgt	21909
Val Ser Asn Ala Val Asn Lys Gln Thr Arg Phe Phe Arg Ser Ala Arg	
1750 1755 1760	
caa tgc tca att cga tat caa atg ttt gtt cgg cca aaa gag ctc gga	21957
Gln Cys Ser Ile Arg Tyr Gln Met Phe Val Arg Pro Lys Glu Leu Gly	
1765 1770 1775 1780	
cag ttg gtg gct tct gat ccg att tcc aag aaa acg atg aaa gtc gac	22005
Gln Leu Val Ala Ser Asp Pro Ile Ser Lys Lys Thr Met Lys Val Asp	
1785 1790 1795	
cta tcg cat act gaa tta tct cat ttg aga aaa gga cga atg act acg	22053
Leu Ser His Thr Glu Leu Ser His Leu Arg Lys Gly Arg Met Thr Thr	
1800 1805 1810	
gag agc caa tat gct cat gat tat gga ata ttg act gat aag aaa cat	22101
Glu Ser Gln Tyr Ala His Asp Tyr Gly Ile Leu Thr Asp Lys Lys His	
1815 1820 1825	
gtg aat aga ttt aaa agt gtt cga gtg gcg gca aca cgg aga cct gtt	22149
Val Asn Arg Phe Lys Ser Val Arg Val Ala Ala Thr Arg Arg Pro Val	
1830 1835 1840	
cag ttt tgg aga ggc cct aaa ggt aga gga gga tgg ctt cat aat agt	22197
Gln Phe Trp Arg Gly Pro Lys Gly Arg Gly Gly Trp Leu His Asn Ser	
1845 1850 1855 1860	
cac tgc aac ttt ttc ctc acg agg gac gag aaa aag tgg ttt cta ggc	22245
His Cys Asn Phe Phe Leu Thr Arg Asp Glu Lys Lys Trp Phe Leu Gly	
1865 1870 1875	
cat ggc cga ggt gcc gac aag ttt ca gcggccattt atcttgcttt	22291
His Gly Arg Gly Ala Asp Lys Phe	
1880	
gttttcgcc cgttttcttt cgtttttcac cgattttttt cgttttttct taataaaact	22351
gataaataaaa tattttttgc agatgctaaa aaaattttcca agtaaaaaaa tcatgtattc	22411
agtgggcatg cagcggtgaa agtgggcatt gtaatatgat ggattacggg tatacaaaac	22471
ctaaactttt tctgaaacat gatacatgtg ctgcttaaat gctgagacta cctgattttc	22531
ataacgagac cgctgaaaaa gttttgaggt ttccaaaatt caactttttt aatqaaaaag	22591

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FIGURE 19

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tcgagatttt cgcacaaaaa gttgaatttt gaaaacctca aaactttttc agcggctctcg 22651
ttatgaaaat caggtaattt cagcatctaa gcatcatatg tatcatgttt cagaaaaagt 22711
taggttttgt attcccgtaa tccatctatt tacattgacc actttcaccg ctgcttgccc 22771
actgaatata taattttttc acttggaat tgttttagca tctggaaaaa gtatttattt 22831
atcagtttta ataagaaaaa acgggaaaaa gctgtgaaaa acaaaaagaaa acaggcggaa 22891
aacaaaagcaa gataaatggc cgtgaaact tgtcggcccc tcggccatgg cctagaaacc 22951
acttttcttc gtccctcgtg aggaaaaagt tgcagtata gtctaaaatt cggaggaatt 23011
ttttaaaatt ggaaaaaatt gttaaatttt tttttctgg aaattggaaa atcacaaatt 23071
ttcgattttt gtttgtaaaa aaaaaaaga aaattggcat aataaaacat ttcttttttt 23131
tttgaaaatt gggaacttct taatatcaga ttttttaagt aagatttttt tgattttccg 23191
gaaattcgga aaacctgaaa attttcaaca ttctaaaata aaaatttccg tttttttttt 23251
ctgaaaatct ccaacaaaaa aaggtcaaat cgtcagaatt attgttgga gtggcggttt 23311
ttcacgatta gatttcagta tttttcttct tgaatttcaa atttgaaaaa aaatcgaata 23371
aaactgtagaa aaatgataga aaattaacaa aaattctgat taaaggtaaa gggaaaatag 23431
accgtaatga ccgaatataa ctgttgaaaa tatcaacaaa aaaaattctg aattttttgt 23491
gactttttca atttttcaag aataaaaaaa acgaccgaat aaaatatttg aattcccgcg 23551
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aaccggcgaa ttagccaga aaacgcaaaa aattaaaaat gacgtcactc atttgccgcg 23671
ggaatacaaa ttaattagg ccgtttcttt gatttttgaa aaattgaaaa aaccattaaa 23731
aaatttagaa atttttttga attttttaca gttttttatt cggtcattat ggggttattc 23791
aagtagtgtc ggaaaattaa aaagtgtaga aaaattacgt cacaactctg tattcaagta 23851
tataaaaaa tgattttaa tacattttgc tacattactt gaataacccc attagggttt 23911
attttcttta gagcaaaaaa aaacatgttt ggctctactc cacctttaa tgaaaaaatc 23971
gacaatttgt gattttgcaa tttccagaaa aaaaagaaaa aagttgcttt ttggaaaaaa 24031
ccaaaaaag ccatttgaaa aattttattt tccaaaaaaa attattttgc agctctagaa 24091
tctcgaaatc tgcaatctct aaacggcgga atgccaccac gacacgagtc gagactcgcc 24151
gaattcgacg taaaaaccaa tattgcctg gacgccgagg acattgtcac aatgtccgac 24211
gagtcgattg tcgcctatga agcagcaag aagaagctac tggccagtcg tcaaacaaaa 24271
ccctcaccac gtcaagatgt ccgattccat acgctgggtc ttcggccgta taccgtacct 24331
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aattcaagtc aaaatccgcc aatacctatc cgacaaatcg gagcagcatc atcacaccaa 24631
catgatcaag gatctcaggg gcctggggga aaaccacaag cctatcacct ggtgcaacag 24691
ggatcacagc aacagcagca gcagcagcag caggcgacgt tacagcgaag aaatgcggcg 24751
gcggcgcgag ggtcgaatgt gcagtttatt cagcagcagc agcagcagca gcaatcgggt 24811
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aacgggaaaa agcgacaatt taaaaaaaaa tcgtgtgaaa atctcaattt tttaacaattt 24931
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acaaaaaaaa atttttgac caaaaaccaa aaacaaaaaa attgaaattt ccgaaaaaatc 25051
aacttaagca tcaaaaattt tttgtttttt tttttgtttt ttggtttttt ttggtatttt 25111
gacgaaaaaa cgattttttg gttttttggt ttttcgagac caaaaaaacc aaaaaatcca 25171
aaaaaatgtt tgccgtgtct agtctcgacc tagacacggc aaacattttt tttttttgga 25231
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tttcgcgcaa tttgatttgt tcgatggagc gcgcttgctt tatttttttt tattcattga 25591
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aaaatgatgc aagcgcgctc caacgaacga attcaattgg cggaaattca aatatggaat 25951
taggtgaaaa ctgagatttt tttttcaatt ttcaaaaaat catataaaat ctagaaccat 26011

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FIGURE 19

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tttttgaatt ttttaatcat gatattcggt cattgtgacc ccataggcgt gtttttaaagc 26071
aatttcccca caggggtgtag tccacctttg acgaggtttg aaaatgtccg gcaatttttg 26131
cgaaattgcc ggaaacttga gattttttcag tgaaaaattc caaattttcat gtggaaaaact 26191
gtttttttgt tttttggaaa atgcaacaaa aaaaactatt tggcgcgaaa acgcggatag 26251
ttttgccaat tttcaaggat tttccgctat ttttaatggt tttatgccga attttacttt 26311
aaaaaatcat aattattcgg aaaatgctcg aagagcattt ccaattgtct gtggagcgcg 26371
tttgactaat cagataatat tccaggcggg caaggacaaa gcttcgttgt catgggctcg 26431
cagagctcat caaatgatgg acaagggtga gcacgcacg tcggaggagg aggaggagga 26491
tcacaacagc ctcaccagca gcagcagcag cagccacaac aaagaatata gtacattcca 26551
caagttaccg gtacggaag taacgggtga ggtggtgga gaggaggcta cggtagtaca 26611
ctggtcatgc caaggaggag acgtgttgtc aggtgtggtg gaaatacaaa atcgcgaaaa 26671
aacggcattt cgggcttccc gaccaatcag cgatttgctc cgccacttt cggaccaatc 26731
cgctgaccga ggcatttgat tggtttgaaa ttggcgagg cagcgaattg ctgatgcgaa 26791
atacggaag ttctcatttt gatggaaatt ctgcaaaatt ctttaaaaaa aacaaaatct 26851
tctcaaattc ggaaaaaatc acaaaggaaa tcgaagaaaa tcgcgatttt tgattccccg 26911
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tggtttgaaa ttggcgagg ctaaaatgat ttttaaaaaa ttcccgattt gtttaatact 27331
gaaattttaga aaaaagaaat atagaaaaaa aatagaaaaa aattaaaaaa aaaaaaaca 27391
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aaaaaactaa aattttaacc aaaaattcaa agaaaaaatt tgtttttgat tttttttcgc 27511
aaaaaaaaaa aaattttaac caaaaattca aaaaaaaaat gtttttcttg atttttttcc 27571
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tttcgaaaaa aaataaaaatt ttaacaaaaa attcaaaaaa aaaatttttt attgactttt 27691
ttcgaaaaaa actcaaattt taaccaaaaa tcaaaaaaaa aaaatttttt ttttgatttt 27751
ttccgaaaaa aactaaaatt ttaacaaaaa attcaaaaaa aaaatgtttt tcttgatttt 27811
tttccaaaaa aactaaaatt ttgacaaaaa attcagcaaa aaaaaaattt ttttaattgat 27871
ttttttttcg aaaaaaata aaattttaac caaaaattca aaaaaaaaat tttttattga 27931
cttttttcga aaaaaactca aattttaacc aaaaattcaa aaaaaaaaat ttttttttg 27991
attttttcgc aaaaaacta aaattttaac caaaaattca aaaaaaaaat tttttattgat 28051
ttttttccaa aaaaactaaa attttgacca aaaattcagc aaaaaaaaaa ttttttaatt 28111
gatttttttt cgaaaaaac taaaattttg accaaaaatt caacaaaaaa aaaatttttt 28171
attgattttt ttcgaaaaaa actaaaattt tgaccaaaaa ttcaacaaaa aaaaattttt 28231
ccagccagcg ggaactctac caggcgggtg acgtctgtat gtcgatcata accgtcatcc 28291
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ggtgttgccg aatcgaggag ctggtggaat tccgcaaatg cgcagtttgc agtgagtttt 28471
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aattgcgaaa ttacacgatt tcgtcttaaa tacggtgcca acctaccca tgacggtttg 28591
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taagagagaa aaataaataa ataatccac aaggttttta aaattttttt ttcaatcgta 28771
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aaaaaaattt ttttaagggt gactacgtc agtggggaaa ttgcttttaa acacgcctat 29191
gaggcccaa tgactgaata tcatgattaa aacaatcaaa aaaaattttc tagattttat 29251
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aattggatta gttcgggtga gcgcgcttac attattttta attattttat ttattttatc 29371
tcgttatttg actgattttt ttcatttttt gtgtgttttc ctcggaaaaa ggaagaaata 29431

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FIGURE 19

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aacaagacaa atgcaaaatg tttgttaaaa agtaattgaa aatgcgtaaa actttgatat 29491
tctgagttcc gacgacaaca agcctgaaat tagtatatct cacagttttt ctcattttca 29551
attacttttt aacaaacatt ttgcatttgt cttgtgtatt tcttccattt tccgaggaaa 29611
aaacatagaa aatgaagaaa atcgggtcaaa taacgagaat aaataaaatt aatttttaaaa 29671
aagatgcaag tgcgctccac cgaacaaatc caattggcgg aaattcaaat atggaattag 29731
gggaaaaactg tgatttttcc cattttcaaa aaatcatata aaatttgga aatttttttg 29791
aattttttta atcatgatata tgggtcattg gcgccccata ggcgtgtttt aaagcaattt 29851
ccccactgag cgtagtccac atttaatttt ccaaaacagc acatgctaata cctccaagtt 29911
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aacgaaaaat tttcgatttt ccaaagaatc gaaaaatcga aaaatgacac ccttgcccc 30871
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taatcggaat attttcgatt ataaaaacgt gtataaaaacg aaaaaaagtg gattttgatg 31591
aaagaaaaaa ttttcttgta gtttttttca gaaaaaaatt actttttatt ctccattttt 31651
tgtttgtgaa tttttgagaa aaaactcatt ttgaaaaaat cgaatttttt atattttttc 31711
taatcgtaaa aaaaaattta aaaatgaatt ccggtaatatt tttaaaaaat aatattaatc 31771
tatagttttg tagttaaaaa aatgtttcac ataaaaatct aaaaaatttt gattttaaat 31831
taaaaaaaat tcgaattttt taaaattttt ttcaaatcgt aaaaaagaa acaataaaca 31891
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tgttttaaat ttgaaaaaaa tataaaaaat tcgatttttt caagataaaa aagcgaattt 32671
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tctgaaatgt tcgatttttt atttttaaaa taatttttaa aaaattttta tattttttat 32791
cgtgcgaatt ttttaccaac tataatttgg aataattttc aqatctcaa aatatccac 32851

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FIGURE 19

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aatcgcgcaa atatgccagg aagcaatgaa gattggataa agaaggaggt cgaggaccag 32911
gacaccaacg ccaacagctc gagctccagc atagccgtct cgcgtcagct cgaagggaat 32971
tctgctgttc ctgacgccat cgaccttctg tcttctcaaa tcaaaagaga agttgaagag 33031
gaggatgata gcaacgatga gactggaccc cgttcggagc ccgtggatgt taagccgtct 33091
ccaaaacgcc caacgaagag gtcagccgag acctggacga cggctcggcg ccaagcaaga 33151
aacggtctac ggcgggagac ggttcaactc atcgattcgc gtatgtgaat gttggagtc 33211
gccatccata cgatccacgc catcttgta tggaaacttc attgaatgaa attaggtaag 33271
gaattattga aaataattat tatatatcca ttttaattca atttttttt tcagaatcga 33331
agatttcgaa ataatccagt atcttccgat gcccttcagg acttcgattc ccatgaagct 33391
agtgatcttc gcagtgaaga gtgaagaatc tgccgagaag atccgctcgt taatcgatcc 33451
ttcgatgttg atcgcggtt ttggtggcgg aaccgaaact caaaaattct tgtggagcga 33511
gctgacgggtg gaggatttcg tcaaggcaca cataatggcc agcaggtaag ctttcgaaca 33571
tacttaattt tttaaaaact aaaattcagc gcaaccgatg acgtgccata tgaggcagcc 33631
atggcggatc gagaatcgct caaacaagct gtaaatgatg ccagctctct gaaaggcttg 33691
aaggaggtaa taatttagaa atgacagaaa atgaaccgtg atgacgaaat acatctgtaa 33751
aaaaattata aaaaattcta agctccgttt ttaattttt ttttcagtta tattctgtca 33811
tagcggccta tttctctgga aaaaaaaatc caaaatagcc tcaaattcgg aattatgctt 33871
cgattttttt tctgcggtag tcttgaattt aagacgattt tgaattttt tagctgctt 33931
tcgcccacat tctgttaaac atttcagagc atgtcgaaaag ctggatggag gatcgtgagt 33991
aagatgcgga aagatctcaa tggagcctga tgatccctt cccagcacac aagacagttt 34051
taattttgtg tctgtatagt tttatattaa gttttgatga taatgaattt ttttacggtt 34111
ttatccatca cttggctcga ttgaagctcc tattgtgcag cacacacggc gtgtaaatta 34171
gtgcatctaa cctaggaaat gcgatttcta ggccatggcc gaggatccga ctatagcttt 34231
tttgatgggtg tttgtacaga gttaaatttc attttgaggg gaaattgaag gaaattgaaa 34291
gagaaattaa ttaataata ttaatttgat ttaaatgacc agaacaaaac aaataaaactg 34351
aatgacaagc caatcgatat tcgtccagac tgggatgatg ttatatgaac tctttcacct 34411
gaaacattta agttttttta ataaaagagc aagcgcgctc aaacgcgaaa acgctcgatc 34471
cacttaattc ggattttgtg ccgattcatt tatttcaagc tatgctcgtt ttttctgtt 34531
atgtttcatt aaaaagaccg aaaaacataac aaaaagtgcc tgaaaacgaa aaaaaaccgg 34591
cgacattaat tgaaaaattc aaaactacaa tttcgcgcc aaaacccaac gagacccaaa 34651
gtttcagcgc ggagcgtttc cacttgccg tggagcgcgc ttgtatataa aaggacttaa 34711
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tgacgggtta ctaaaatatg ctccaaatag ttggcaaggc gttgacttga ataaatcggg 34831
atggttatct tggatgattg cagttcgatt tccttttgta attatgttct aaaaagtcatt 34891
tgtaatcatt taaaagtggg gtagcgccag tggggatttt gtctaaatgc acttattatg 34951
atccaaaaca accgaatata atcataaaac actccaaaaa gtttagtttt ttcataattt 35011
cctgtcaaaag ttttgcaaa ttggcaaaat tttgaaaaat gcgagctttt gaggtaattt 35071
aaggaaatgt cgcagtgttc gacccctaca attatttaat acagataatt taaacaaaat 35131
taaaaacataa aaatgtagaa atttttttt ttttggtcga tttccaaaat tatgagtggc 35191
aaaaactgag taattgccac tttttgacag taaataaaaa atgttcaaaa ttttttgaaa 35251
cgttttatca tgatatttgg ccattatggg agcaaatgag tggtttatct attttttcac 35311
tggcgctact ccacctttaa gcatgtctgc ctaccataa tccatttaa tccaacgttt 35371
cttagatttg gattcgaata tatttgaatg actggaaaat atgttacgtt accattcaat 35431
gcaccaatat aagtcatttg atcgagaaaa ttcaaatcgg tgagatttgt gtttctgata 35491
gtcaatgttc cgaataaaaa ttgtaacact cctaatttgg aaacataatt ttcattctca 35551
tggcttatta atagatctcc aaggatatac atacatgtat ctgatagttt gctcatgtat 35611
tcaaatgtgc aataaaatga cgcattcaat ggaccaggat ctttgcaaag tttcgttcca 35671
atgttttcag tagaaattcc aaggttcaat agggcaacta tctcagtaat ggtgacacaa 35731
aaatcaggat gaaggttttc aaaattgaag tattgccttt tattgtatgt actgtattgt 35791
atcatactgg tttgctcaac tgtatctata actttctgaa attttatgtc attattttca 35851
gaaatcgac taggcaggca agcctgcctt accgtcagaa ttggcagtc cagtcgaatc 35911
atttcggat tatctgtac attcaatgct acactagcta tatccgagtt atattcgata 35971
gtttcgaggt tttgtaaaaa cgacaaactc tgtagattag tgttccgaat tgcaatagat 36031
cctcgaatca ttgtgacatt caaaaatgaa tcataatcga aggttgcat aatattcact 36091
aaatttagac cagaatctag agttttgcat ttggagtact ccttaacatt tgatacatta 36151
actttttcac catcacatcc tgaaatttga ctatttttat actgttaaaa aattgtttct 36211
caccacaatc ctttaagttc cctctgacaa tgagctcatt atacatgtgt aaaaqccgc 36271

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FIGURE 19

```

catcacagga aaattccagt ttcggattat tctcgattct aatcacac gcctcgatac 36331
cccgatcacg gtacaagtag agatcgtaga gcacactggg gtcgtttaat tgtgaattgt 36391
ttcggatgta aacaccgtct gaaatctgaa gtttaagaaa aaattaagta agttttaatc 36451
tacatggtga tccgtttttg ttgaaagtat caaaaaatta actggagtca gaatgtctca 36511
tttcgttttg atcttcaaaa aatgcgggag ttcagacctt gacatctcgt ctgatttcgc 36571
atggttaaga gcgttctgac gtcacaattt ttctgaaaaa atattccgcg attttttgta 36631
gatcaaatta aaatgagaca gcctgacacc acgtggagtt ccttatatac aaaaaagttg 36691
atttttcgct cgtgattttt cgttgtaaca tcatgaaaaa tccagtgttc tctgcaaacc 36751
actaaaatcc acttttttgt ttcagccgct ccgcaagcag cttcgtcgag gtcatggcag 36811
cggccgagtt tcccactccg ctgaaactcg gcacttaata tatgaacgac taagctagca 36871
gggccgccat tctaccttac cagcaaaaat gaattcgttc acttacacac atcacacacc 36931
acattaaagt ttcctttttc tttgtcagct gtaaaaaccg aaaggcttgt cagactagta 36991
ttctcaatat taaatc 37007

```

FIGURE 20A

ssl-1 Predicted exons:

Exon	Position in genomic sequence (inclusive)
1	1001-1281
2	1923-2027
3	2084-2312
4	4420-5205
5	5855-6487
6	7685-8515
7	9700-10184
8	12211-13165
9	13643-13726
10	13796-13939
11	18879-19101
12	20449-20735
13	21661-22273

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Figure 20B

ssl-1 cDNA

```

atgccggcaa caccggtgcg tgcttcaagt actcgaataa gcagacgtac atcatcaaga 60
tcagtggctg atgatcagcc atcaacttcg tctgcggtgg ctccacctcc ttcacccatt 120
gccatagaaa ctgatgaaga tgcggtagtt gaggaggaga aaaagaagaa aaagacatca 180
gatgatttgg aaattatcac tccaagaact ccagtcgata ggcaattccc ctacatttgc 240
tcgattcttt tgactgaaaa tcgatcgatt cgcgataaat tggttctgag cagcgggtcca 300
gttcgtcaag aagatcacga agaacagatt gctcagctc aacggataca gccagttgtc 360
gatcaaattc aacgagtcga gcaaatcata ctcaatggtt cagtgggaaga tattctgaaa 420
gatcctcgat tcgcagtaat ggcagatctc acaaaagaac caccaccaac acctgcacct 480
cctcctccaa tccagaagac aatgcaaccg attgaggtga aaattgagga ttcagagggc 540
tcaaatacgg ctcaaccgag tgttctgccc agttgtggag gaggagagac gaatgtggaa 600
agagccgcca aaagagaagc gcatgtattg gctcgaatcg ccgagctccg taagaacggc 660
ttatgggtcga acagtcgtct gccaaagtgc gtcgaacctg aacgtaataa aacgcattgg 720
gattatctac tggaagaggt caaatggatg gcagttgatt tccgaaccga gacgaatacg 780
aagcgaaaaa tcgccaaaagt tatagctcac gccattgcga aacagcaccg cgacaagcag 840
atcgagattg agagagccgc cgaacgggag atcaaaggaga agcgaaaaaat gtgtgcagga 900
atcgcgaaaga tggtagcgga tttctggctg gctcaggaag tctacggata aagttgtgga tattcgagcg 960
aagggaagttc tggagtcgag gctcaggaag gcgagaaata agcatttgat gtttgtaatt 1020
ggacaagtgc atgaaatgag caatattgtg caagaaggac ttgtttcatc gtcgaaatcc 1080
ccatcaattg catcggatcg agatgataaa gatgaagaat tcaaagcacc tggctctgat 1140
tcagaattcg acgatgagca gacaattgca aacgcggaaa agtcacagaa aaaggaagat 1200
gttcgacagg aagttgatgc tcttcaaaac gaggcaactg tggatatgga tgactttttg 1260
tacactttac cgccggaata tctgaaggct tatggctctga cgcaggagga tttggaggag 1320
atgaagcgcg agaaattgga ggagcagaag gctcgggaag aagcttgtgg tgataatgag 1380
gagaaaaatg agattgatga aagcccatca tcagatgctc aaaagccttc cacctcaagc 1440
tcagatctca ccgccgagca gtttcaagat ccaacagctg aagacggcaa cgggtgatggt 1500
catggtgtac ttgaaaacgt ggattacgtg aaagctcaaca gtcaggatag tgatgaacga 1560
caacaagagt tggcgaatat cgcagaagaa gcgctgaaat tccagccaaa aggatataca 1620
cttgagacga cacaagtcaa gacgcccgtg ccattcctga ttcgaggaca actgagagaa 1680
tatcaaatgg ttggattgga ttggatgggt acactttatg agaagaattt gaattggaatt 1740
cttccgacg agatgggctt gggaaagacg attcaaacga tttccctgct ggctcatatg 1800
gcttgtagt aatcgatttg gggaccacac ttgattgttg tgccgacgtc tgtcattctg 1860
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acggcgaagg agcgtgccga gaagcgggaag ggatggatga agccgaattg tttccatgtg 1980
tgcatcacat catacaagac ggttactcaa gatattagag cttttaagca gagggcctgg 2040
cagtacctaa ttctcgatga agctcaaaat atcaaaaaact ggaagtccca acgttggcag 2100
gctcttctga atgtccgtgc tcgacgtcgc cttctcctga ccggaactcc acttcagaac 2160
tctctaattg aactgtggtc gttgatgcat tttttgatgc caacaatatt ctcaagtcac 2220
gatgatttca aggattggtt ctggaatccg ttgacaggga tgatgggaag aaatatggaa 2280
ttcaatgctc cactaatcgg acgacttcac aaagtgtccc gtcggtttat tctgcggcgg 2340
ctcaagaagg aagttgagaa gcagctgccg gagaagactg agcatattgt gaattgttcg 2400
ttgtcaaaagc ggcagagata cctgtacgat gactttatga gtcgtagatc aacaaaggag 2460
aatctaaagt ctggaaatat gatgtcggtg ctcaacattg tgatgcaact ccgaaaaatgt 2520
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ggaacagctc aaccacttca aaatggaaat tcaataccac aaaatgctcc aaatcgtcca 2940
caaaacttcat gcattcggtc aaaaaccgtc gtaaatcacag ttccactgac catctccacc 3000
gatcgaagtg gttttcattt taatatggcc aatgttggaag gaggtgttgt tcggttggtt 3060
gattcagcac gtatgagccc accgctcaaa cgtcagaagc tcaccggaac tgcaacgaat 3120

```

Figure 20B

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tggagtgatt atgttccgcg acacgttggt gaaaagatgg aagaatcgag aaaaaaccag 3180
ctggaaaattg ttcgaaggcg atttgagatg attcgtgctc cgattattcc actggaaatg 3240
gttgcgctgg ttcgagagga aattattgca gaatttccac gtttggtgtt ggaagaggac 3300
gagggtgtgc aggagaggct tttggagtat tgcgagtgtt tgggtgcaaag attcggaatg 3360
tacgtcgaac cagtgtgac cgatgcttgg cagtgtcgtc catcatcgtc tggctctcca 3420
tcatatattc gcaacaattt atcaaatac gagctgaatt ctcttctct tctcctcaac 3480
acctccacta atttcgatac ccgaatgtcg atctcacgtg ctcttcaatt cccagaactc 3540
cgtctgatcg agtacgattg tggaaagctt cagacgttgg ctgttctgct tcgtcagttg 3600
tacctgtaca agcacagatg tctgatcttc acgcaaatgt caaagatgct cgacgttctg 3660
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tacgattcgg attggaatcc gacgatggat gctcaggctc aggatagatg tcatcgatc 3900
ggacagacga ggaatgtctc gatttatcga ttgatttccg agcgaacaat tgaggagaat 3960
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gcgatggcaa agtgtgaaga tgaagctgat gtgaatgcgg cgaagattgc ggtggccgag 4200
gcgaacgttg ataatgcgga gtttgatgag aaatcattgc cgccgatgag caatttgcaa 4260
ggagatgagg aggtgatga gaagtatatg gatttgatac aacagctcaa accaatcgaa 4320
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ttgaatgcgt ttaatgacat tctatcggca aaagaaaagg aatcgggtga cgatgcggtc 4800
aacaagtgcc ttcaaatgcc acaatccgaa gcgatcacag cagaatctgc agcgtctcca 4860
gcatacacgg aacactcatc attctcgatg gatgatacaa gccaggatgc gaagattgag 4920
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acggctcaaa atcgaacagc tgaaaatggg gtgaaacgag cgacaactcc accaccatca 5100
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cactgcaact ttttcctcac gagggacgag aaaaagtggg ttctaggcca tggccgaggt 5640
gccgacaagt ttcagc 5656

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FIGURE 21

ssl-1 protein

<400> 3

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Met Pro Ala Thr Pro Val Arg Ala Ser Ser Thr Arg Ile Ser Arg Arg
 1           5           10           15
Thr Ser Ser Arg Ser Val Ala Asp Asp Gln Pro Ser Thr Ser Ser Ala
      20           25           30
Val Ala Pro Pro Pro Ser Pro Ile Ala Ile Glu Thr Asp Glu Asp Ala
      35           40           45
Val Val Glu Glu Glu Lys Lys Lys Lys Thr Ser Asp Asp Leu Glu
      50           55           60
Ile Ile Thr Pro Arg Thr Pro Val Asp Arg Arg Ile Pro Tyr Ile Cys
      65           70           75           80
Ser Ile Leu Leu Thr Glu Asn Arg Ser Ile Arg Asp Lys Leu Val Leu
      85           90           95
Ser Ser Gly Pro Val Arg Gln Glu Asp His Glu Glu Gln Ile Ala Arg
      100          105          110
Ala Gln Arg Ile Gln Pro Val Val Asp Gln Ile Gln Arg Val Glu Gln
      115          120          125
Ile Ile Leu Asn Gly Ser Val Glu Asp Ile Leu Lys Asp Pro Arg Phe
      130          135          140
Ala Val Met Ala Asp Leu Thr Lys Glu Pro Pro Thr Pro Ala Pro
      145          150          155          160
Pro Pro Pro Ile Gln Lys Thr Met Gln Pro Ile Glu Val Lys Ile Glu
      165          170          175
Asp Ser Glu Gly Ser Asn Thr Ala Gln Pro Ser Val Leu Pro Ser Cys
      180          185          190
Gly Gly Gly Glu Thr Asn Val Glu Arg Ala Ala Lys Arg Glu Ala His
      195          200          205
Val Leu Ala Arg Ile Ala Glu Leu Arg Lys Asn Gly Leu Trp Ser Asn
      210          215          220
Ser Arg Leu Pro Lys Cys Val Glu Pro Glu Arg Asn Lys Thr His Trp
      225          230          235          240
Asp Tyr Leu Leu Glu Glu Val Lys Trp Met Ala Val Asp Phe Arg Thr
      245          250          255
Glu Thr Asn Thr Lys Arg Lys Ile Ala Lys Val Ile Ala His Ala Ile
      260          265          270
Ala Lys Gln His Arg Asp Lys Gln Ile Glu Ile Glu Arg Ala Ala Glu
      275          280          285
Arg Glu Ile Lys Glu Lys Arg Lys Met Cys Ala Gly Ile Ala Lys Met
      290          295          300
Val Arg Asp Phe Trp Ser Ser Thr Asp Lys Val Val Asp Ile Arg Ala
      305          310          315          320
Lys Glu Val Leu Glu Ser Arg Leu Arg Lys Ala Arg Asn Lys His Leu
      325          330          335
Met Phe Val Ile Gly Gln Val Asp Glu Met Ser Asn Ile Val Gln Glu
      340          345          350
Gly Leu Val Ser Ser Ser Lys Ser Pro Ser Ile Ala Ser Asp Arg Asp
      355          360          365
Asp Lys Asp Glu Glu Phe Lys Ala Pro Gly Ser Asp Ser Glu Ser Asp
      370          375          380
Asp Glu Gln Thr Ile Ala Asn Ala Glu Lys Ser Gln Lys Lys Glu Asp
      385          390          395          400
Val Arg Gln Glu Val Asp Ala Leu Gln Asn Glu Ala Thr Val Asp Met
      405          410          415

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FIGURE 21

Asp	Asp	Phe	Leu	Tyr	Thr	Leu	Pro	Pro	Glu	Tyr	Leu	Lys	Ala	Tyr	Gly
		420						425					430		
Leu	Thr	Gln	Glu	Asp	Leu	Glu	Glu	Met	Lys	Arg	Glu	Lys	Leu	Glu	Glu
		435					440					445			
Gln	Lys	Ala	Arg	Lys	Glu	Ala	Cys	Gly	Asp	Asn	Glu	Glu	Lys	Met	Glu
	450					455					460				
Ile	Asp	Glu	Ser	Pro	Ser	Ser	Asp	Ala	Gln	Lys	Pro	Ser	Thr	Ser	Ser
465					470					475					480
Ser	Asp	Leu	Thr	Ala	Glu	Gln	Leu	Gln	Asp	Pro	Thr	Ala	Glu	Asp	Gly
			485						490					495	
Asn	Gly	Asp	Gly	His	Gly	Val	Leu	Glu	Asn	Val	Asp	Tyr	Val	Lys	Leu
		500						505					510		
Asn	Ser	Gln	Asp	Ser	Asp	Glu	Arg	Gln	Gln	Glu	Leu	Ala	Asn	Ile	Ala
		515					520					525			
Glu	Glu	Ala	Leu	Lys	Phe	Gln	Pro	Lys	Gly	Tyr	Thr	Leu	Glu	Thr	Thr
	530					535					540				
Gln	Val	Lys	Thr	Pro	Val	Pro	Phe	Leu	Ile	Arg	Gly	Gln	Leu	Arg	Glu
545					550					555					560
Tyr	Gln	Met	Val	Gly	Leu	Asp	Trp	Met	Val	Thr	Leu	Tyr	Glu	Lys	Asn
				565					570					575	
Leu	Asn	Gly	Ile	Leu	Ala	Asp	Glu	Met	Gly	Leu	Gly	Lys	Thr	Ile	Gln
		580						585					590		
Thr	Ile	Ser	Leu	Leu	Ala	His	Met	Ala	Cys	Ser	Glu	Ser	Ile	Trp	Gly
		595					600					605			
Pro	His	Leu	Ile	Val	Val	Pro	Thr	Ser	Val	Ile	Leu	Asn	Trp	Glu	Met
	610					615					620				
Glu	Phe	Lys	Lys	Trp	Cys	Pro	Ala	Leu	Lys	Ile	Leu	Thr	Tyr	Phe	Gly
625					630					635					640
Thr	Ala	Lys	Glu	Arg	Ala	Glu	Lys	Arg	Lys	Gly	Trp	Met	Lys	Pro	Asn
				645					650					655	
Cys	Phe	His	Val	Cys	Ile	Thr	Ser	Tyr	Lys	Thr	Val	Thr	Gln	Asp	Ile
		660						665					670		
Arg	Ala	Phe	Lys	Gln	Arg	Ala	Trp	Gln	Tyr	Leu	Ile	Leu	Asp	Glu	Ala
		675					680					685			
Gln	Asn	Ile	Lys	Asn	Trp	Lys	Ser	Gln	Arg	Trp	Gln	Ala	Leu	Leu	Asn
	690					695					700				
Val	Arg	Ala	Arg	Arg	Arg	Leu	Leu	Leu	Thr	Gly	Thr	Pro	Leu	Gln	Asn
705					710					715					720
Ser	Leu	Met	Glu	Leu	Trp	Ser	Leu	Met	His	Phe	Leu	Met	Pro	Thr	Ile
				725					730					735	
Phe	Ser	Ser	His	Asp	Asp	Phe	Lys	Asp	Trp	Phe	Ser	Asn	Pro	Leu	Thr
			740					745					750		
Gly	Met	Met	Glu	Gly	Asn	Met	Glu	Phe	Asn	Ala	Pro	Leu	Ile	Gly	Arg
		755					760					765			
Leu	His	Lys	Val	Leu	Arg	Pro	Phe	Ile	Leu	Arg	Arg	Leu	Lys	Lys	Glu
	770					775					780				
Val	Glu	Lys	Gln	Leu	Pro	Glu	Lys	Thr	Glu	His	Ile	Val	Asn	Cys	Ser
785					790					795					800
Leu	Ser	Lys	Arg	Gln	Arg	Tyr	Leu	Tyr	Asp	Asp	Phe	Met	Ser	Arg	Arg
			805						810					815	
Ser	Thr	Lys	Glu	Asn	Leu	Lys	Ser	Gly	Asn	Met	Met	Ser	Val	Leu	Asn
			820					825					830		
Ile	Val	Met	Gln	Leu	Arg	Lys	Cys	Cys	Asn	His	Pro	Asn	Leu	Phe	Glu
		835					840					845			
Pro	Arg	Pro	Val	Val	Ala	Pro	Phe	Val	Val	Glu	Lys	Leu	Gln	Leu	Asp
	850					855				860					
Val	Pro	Ala	Arg	Leu	Phe	Glu	Ile	Ser	Gln	Gln	Asp	Pro	Ser	Ser	Ser

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865	870	875	880
Ser Ala Ser Gln Ile Pro Glu Ile Phe Asn Leu Ser Lys Ile Gly Tyr			
	885	890	895
Gln Ser Ser Val Arg Ser Ala Lys Pro Leu Ile Glu Glu Leu Glu Ala			
	900	905	910
Met Ser Thr Tyr Pro Glu Pro Arg Ala Pro Glu Val Gly Gly Phe Arg			
	915	920	925
Phe Asn Arg Thr Ala Phe Val Ala Lys Asn Pro His Thr Glu Glu Ser			
	930	935	940
Glu Asp Glu Gly Val Met Arg Ser Arg Val Leu Pro Lys Pro Ile Asn			
	945	950	955
Gly Thr Ala Gln Pro Leu Gln Asn Gly Asn Ser Ile Pro Gln Asn Ala			
	965	970	975
Pro Asn Arg Pro Gln Thr Ser Cys Ile Arg Ser Lys Thr Val Val Asn			
	980	985	990
Thr Val Pro Leu Thr Ile Ser Thr Asp Arg Ser Gly Phe His Phe Asn			
	995	1000	1005
Met Ala Asn Val Gly Arg Gly Val Val Arg Leu Asp Asp Ser Ala Arg			
	1010	1015	1020
Met Ser Pro Pro Leu Lys Arg Gln Lys Leu Thr Gly Thr Ala Thr Asn			
	1025	1030	1035
Trp Ser Asp Tyr Val Pro Arg His Val Val Glu Lys Met Glu Glu Ser			
	1045	1050	1055
Arg Lys Asn Gln Leu Glu Ile Val Arg Arg Arg Phe Glu Met Ile Arg			
	1060	1065	1070
Ala Pro Ile Ile Pro Leu Glu Met Val Ala Leu Val Arg Glu Glu Ile			
	1075	1080	1085
Ile Ala Glu Phe Pro Arg Leu Ala Val Glu Glu Asp Glu Val Val Gln			
	1090	1095	1100
Glu Arg Leu Leu Glu Tyr Cys Glu Leu Leu Val Gln Arg Phe Gly Met			
	1105	1110	1115
Tyr Val Glu Pro Val Leu Thr Asp Ala Trp Gln Cys Arg Pro Ser Ser			
	1125	1130	1135
Ser Gly Leu Pro Ser Tyr Ile Arg Asn Asn Leu Ser Asn Ile Glu Leu			
	1140	1145	1150
Asn Ser Arg Ser Leu Leu Leu Asn Thr Ser Thr Asn Phe Asp Thr Arg			
	1155	1160	1165
Met Ser Ile Ser Arg Ala Leu Gln Phe Pro Glu Leu Arg Leu Ile Glu			
	1170	1175	1180
Tyr Asp Cys Gly Lys Leu Gln Thr Leu Ala Val Leu Leu Arg Gln Leu			
	1185	1190	1195
Tyr Leu Tyr Lys His Arg Cys Leu Ile Phe Thr Gln Met Ser Lys Met			
	1205	1210	1215
Leu Asp Val Leu Gln Thr Phe Leu Ser His His Gly Tyr Gln Tyr Phe			
	1220	1225	1230
Arg Leu Asp Gly Thr Thr Gly Val Glu Gln Arg Gln Ala Met Met Glu			
	1235	1240	1245
Arg Phe Asn Ala Asp Pro Lys Val Phe Cys Phe Ile Leu Ser Thr Arg			
	1250	1255	1260
Ser Gly Gly Val Gly Val Asn Leu Thr Gly Ala Asp Thr Val Ile Phe			
	1265	1270	1275
Tyr Asp Ser Asp Trp Asn Pro Thr Met Asp Ala Gln Ala Gln Asp Arg			
	1285	1290	1295
Cys His Arg Ile Gly Gln Thr Arg Asn Val Ser Ile Tyr Arg Leu Ile			
	1300	1305	1310
Ser Glu Arg Thr Ile Glu Glu Asn Ile Leu Arg Lys Ala Thr Gln Lys			
	1315	1320	1325

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FIGURE 21

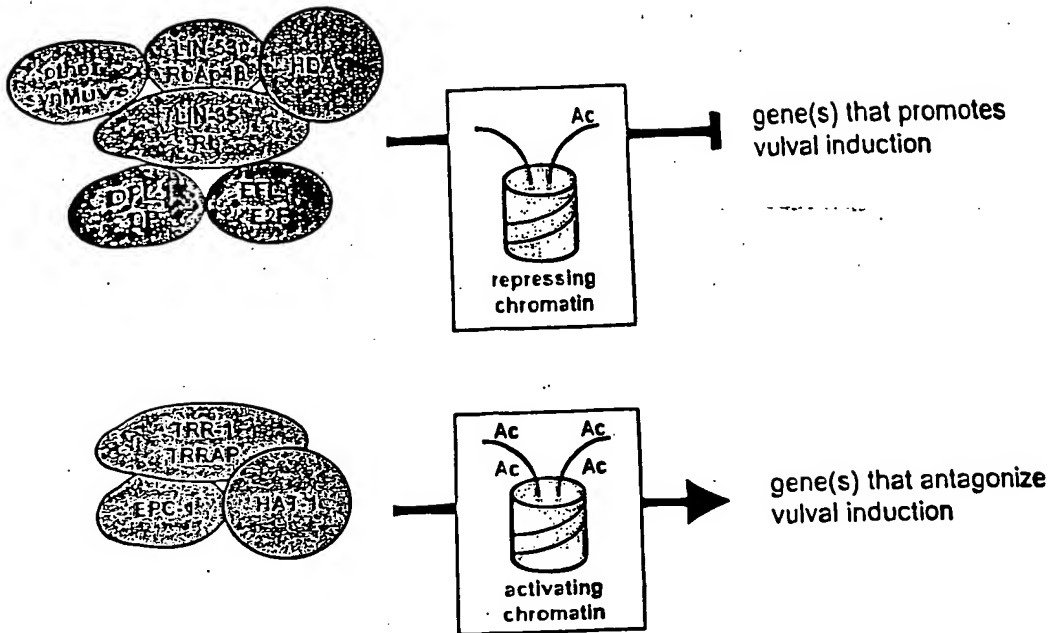
Arg Arg Leu Gly Glu Leu Ala Ile Asp Glu Ala Gly Phe Thr Pro Glu
 1330 1335 1340
 Phe Phe Lys Gln Ser Asp Ser Ile Arg Asp Leu Phe Asp Gly Glu Asn
 1345 1350 1355 1360
 Val Glu Val Thr Ala Val Ala Asp Val Ala Thr Thr Met Ser Glu Lys
 1365 1370 1375
 Glu Met Glu Val Ala Met Ala Lys Cys Glu Asp Glu Ala Asp Val Asn
 1380 1385 1390
 Ala Ala Lys Ile Ala Val Ala Glu Ala Asn Val Asp Asn Ala Glu Phe
 1395 1400 1405
 Asp Glu Lys Ser Leu Pro Pro Met Ser Asn Leu Gln Gly Asp Glu Glu
 1410 1415 1420
 Ala Asp Glu Lys Tyr Met Glu Leu Ile Gln Gln Leu Lys Pro Ile Glu
 1425 1430 1435 1440
 Arg Tyr Ala Ile Asn Phe Leu Glu Thr Gln Tyr Lys Pro Glu Phe Glu
 1445 1450 1455
 Glu Glu Cys Lys Glu Ala Glu Ala Leu Ile Asp Gln Lys Arg Glu Glu
 1460 1465 1470
 Trp Asp Lys Asn Leu Asn Asp Thr Ala Val Ile Asp Leu Asp Asp Ser
 1475 1480 1485
 Asp Ser Leu Leu Leu Asn Asp Pro Ser Thr Ser Ala Asp Phe Tyr Gln
 1490 1495 1500
 Ser Ser Ser Leu Leu Asp Glu Ile Lys Phe Tyr Asp Glu Leu Asp Asp
 1505 1510 1515 1520
 Ile Met Pro Ile Trp Leu Pro Pro Ser Pro Pro Asp Ser Asp Ala Asp
 1525 1530 1535
 Phe Asp Leu Arg Met Glu Asp Asp Cys Leu Asp Leu Met Tyr Glu Ile
 1540 1545 1550
 Glu Gln Met Asn Glu Ala Arg Leu Pro Gln Val Cys His Glu Met Arg
 1555 1560 1565
 Arg Pro Leu Ala Glu Lys Gln Gln Lys Gln Asn Thr Leu Asn Ala Phe
 1570 1575 1580
 Asn Asp Ile Leu Ser Ala Lys Glu Lys Glu Ser Val Tyr Asp Ala Val
 1585 1590 1595 1600
 Asn Lys Cys Leu Gln Met Pro Gln Ser Glu Ala Ile Thr Ala Glu Ser
 1605 1610 1615
 Ala Ala Ser Pro Ala Tyr Thr Glu His Ser Ser Phe Ser Met Asp Asp
 1620 1625 1630
 Thr Ser Gln Asp Ala Lys Ile Glu Pro Ser Leu Thr Glu Asn Gln Gln
 1635 1640 1645
 Pro Thr Thr Thr Ala Thr Thr Thr Thr Val Pro Gln Gln Gln Gln
 1650 1655 1660
 Gln Gln Gln Gln Gln Lys Ser Ser Lys Lys Lys Arg Asn Asp Asn Arg
 1665 1670 1675 1680
 Thr Ala Gln Asn Arg Thr Ala Glu Asn Gly Val Lys Arg Ala Thr Thr
 1685 1690 1695
 Pro Pro Pro Ser Trp Arg Glu Glu Pro Asp Tyr Asp Gly Ala Glu Trp
 1700 1705 1710
 Asn Ile Val Glu Asp Tyr Ala Leu Gln Ala Val Gln Val Glu Phe
 1715 1720 1725
 Ala Asn Ala His Leu Val Glu Lys Ser Ala Asn Glu Gly Met Val Leu
 1730 1735 1740
 Asn Trp Glu Phe Val Ser Asn Ala Val Asn Lys Gln Thr Arg Phe Phe
 1745 1750 1755 1760
 Arg Ser Ala Arg Gln Cys Ser Ile Arg Tyr Gln Met Phe Val Arg Pro
 1765 1770 1775
 Lys Glu Leu Gly Gln Leu Val Ala Ser Asp Pro Ile Ser Lys Lys Thr

FIGURE 21

	1780		1785		1790
Met	Lys	Val	Asp	Leu	Ser
	1795		1800		1805
Arg	Met	Thr	Thr	Glu	Ser
	1810		1815		1820
Asp	Lys	Lys	His	Val	Asn
	1825		1830		1835
Arg	Arg	Pro	Val	Gln	Phe
			1845		1850
Leu	His	Asn	Ser	His	Cys
			1860		1865
Trp	Phe	Leu	Gly	His	Gly
			1875		1880
					1885

FIGURE 22

A)



B)

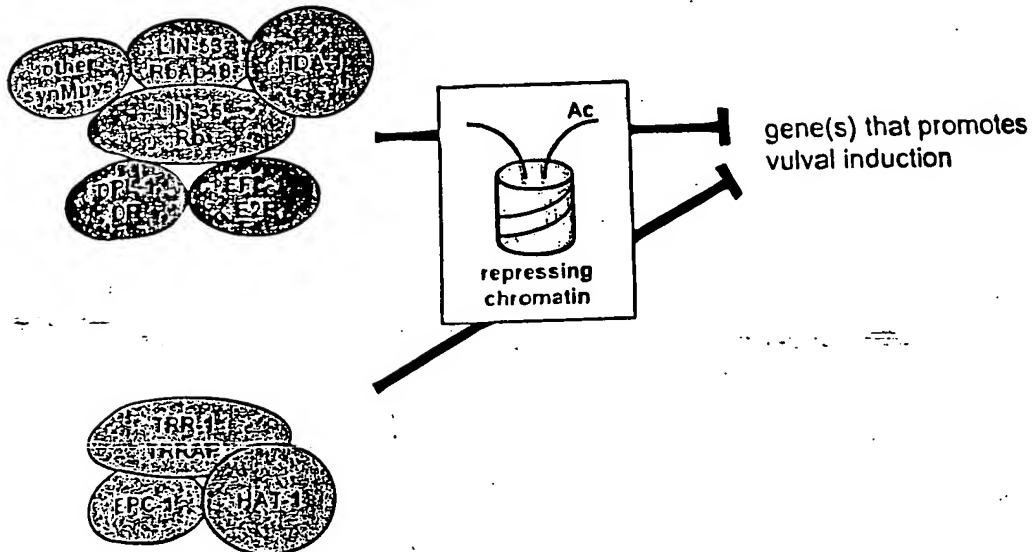


Figure 23

lin(n3628) genomic sequence (1 kb of upstream and downstream genomic sequence is included in this file).

<u>Exon number</u>	<u>Exon boundaries (inclusive)</u>
1	1001 – 1035
2	1920 – 2062
3	2114 – 2190
4	2241 – 2501
5	2551 – 2903
6	2955 – 3405
7	3497 – 3631
8	4227 – 4690
9	5293 – 6058
10	6696 – 7058
11	7609 – 8338
12	8771 – 8933
13	9511 – 10306
14	10774 – 10851

GTCAATGGAATTCTCGACGCGGATCTTGTTAGAGATGCCGTCGAGAGAGATT
 TGATCAAATTGCGGTACGCTGAAACGGATGCACCAGTTTTACAGGTAAAATG
 GAAATATACAACTCAAAAGTAAAATTTTATGAATTTTCAGATCAACAACTCA
 CTATACACGGCATCCTGGGAGCAAGATCTCGGAACAAATATGGTTCTGCAGT
 CAAAAGGAAAAGAGATGGAAGTGATTTTCGTGTACATCGACCATGATGACTGC
 AGAAAAAGCCCTGTTGACCTCGTTAAGCACCGAAGGATCTACACTAGCCGCC
 AATGCAGAGACTGCTCCGAAATCTGATCTCAGTCGAACTCAACCACGTCAAC
 AATGATTTTCAAAATATAAATTAACATGAAGCTCTGAAATAAACTCATATAA
 CTGCTAAAATAAACTGTTGCTTTTGAACCAACATTTGTTAGACAACCTGCG
 TCTCACAGTCATTTTTCAATATATTGGCGCCGCGCACACACAAAGAAGAAGA
 ATTCGTCCTCATGGCATGGCATGTGCAGTCAGCGGCCACCCTGTGTAACCACT
 GCGTATCGCATCTTTCCACGTGTTTTTGCAATCTTGCTGTACGTTTCAATTCCT
 CGTACAACCATCTCTTCTACCCCGTTGCCTCCTCCACCATCTCATCTCAATTG
 TGTCGTTGCCCTCCCTCTCCCCAAGTCTTTCTGCGTCTCTTAGTGCTCTTCGAG
 AAAAGAACGAGGAGAGCTGTGAGACGCTAGTAGGAAACGCATTCTCAATTC
 GATATAGGCACATTGAGAGAGAGCGAGCGCCGTTTCGACGTCTTCTAGCCTT
 CACATCATCCAGACGACGTTACACGCACACACAGCCAACCCCACTTCTG
 ACAACGAATAGACGACGAAGAAGAGAAGAAGAAAAAGAAGGTACCCA
 TTTTTCATTCCCTTTTTGCCTCCACACTTCACTATTATCGATTTTGTGAGCGAG
 CTCTAATGTTTCAACGCAAAGTGGTATTGCCTAAAAAGCGGTGAGAATTTGCT
 TCAGACAGAAATTCGTTTTTTTAAACAAGAAAAATCCGGTTTCAATTGTCGTA
 GAAGGTCAATTTTTACTTTCAACGCTCTTCATTGACGGAAAACGTTTTTCTT
 TCAAATTTTAAATTACAGAGGCATTTTACTCAAGGTTTGTTTTAAATTAAATT
 AAAAATAAATTTTAAAATAGAAATATGGATAATATAAAATGTTTTCTTCAA
 AAATGCACTCAGGTTTACCAAAAAATCGATAATTAAAAATACGGTCGCAAAG
 GAGCGTCGTTAGCTGCTAATCAATGGTCTTAAAACGAAATCTATCGATTTTTG
 TGTACTACACACGGACAAGTGCTCCACCGTTATTTTTTTGAACGAGTGCGTTGC

FIGURE 23

AATTCCATCCCATTTTGACGTTTTTCTTTTTTTTTTCATCAAATTTTTTAGCATT
TAAAGTAAAGTCAATGATAACCTGCAAATAATAATGTAAAATTCATTAAAAA
CCGAGAGAAAAAGTCTAAAGTCATAAATTTTTGATAAAAAAGTGATTTTCGA
AACTAAAAATCATTCAAATTAAGTTGAACCTGATTCTTCAATTTTTATTATA
TATTAAGGCTTGATCCACTCAAATAAAAGGAGTTTTTAATTGAGAAAAAAA
GCAAATGAAAAAATCGATAATTAATTTGGGCGCCAACCTAGATTTTAATATG
TTTTTGTTAGAAATTTGTATATTTTCATCACTCTCTGACTTTAAGCATTCGTAT
TTTAAGGAAGTGTGAGCTTTCTAATATGTTTTTTATTAAAAAAACATGTTTT
TAACAATCTCCCTGTCATCCCCATCACCTAATGCACTCAAATAATCAATAATC
ACAATACTTTTATTTTTTTCTTGACAGAACAGAAATGGTCCAAACGAGACGAAA
GACAGCTGCAGCTGTACAGGACGGTGGTGCCGTTAAGGAGAACAAAGCCAA
GCCACCTGCCCTCAAACGCCTACAAAACGAGCAAAACGAGGTCGTCCCCCG
AAAATTAAGACTGGTGAGCGAATGACTATACGGAAGATTGAAAATTCACGTG
GAATACTTGACAGATGCCAATACTTTGAATACGCCAAGCACTTCTTCCAACCTG
GTCGATGACAAACTTCTCATTGAGTCTGAATCACAGGTAAATTGATTCTTTTC
TATTCAAAAATTAATCTAAACTATACATTCCAGGACTCGATTCTCACAAACGA
AGCCGACTCTTTTCTGGAAAAAGAAGTGGAAGAAATCGAAGATAGTTCAGAT
ATACTTCCCGATAAAATTAATTCTCCAGAAAAACCAAGTGTTTTGGTGAAGC
GGAGATCGAGTACGCGGTTAAAAGTGAAGACTGATGAAGATGAAAAAGATG
TTCCTGTGAACATAGAAGTAGCCGTTTTAGAAGAAAAATCAATTCAAATCGA
GCCAACATCTCCCGCTCACCCGGAAGATCCTCAGGTGAGCTTTTTTTAAAAAT
ATGTATTAATCAAAATTCCTTCATTTCAGCCTTCGACTTCTTCTCTTCCACTG
GTAGAACCAATTGAAGACATTGTGGAGCCAAATGAGCCAACAAGCTCTGCCG
ATCCTCCAGTATCAAATATTAAGGATGAGGATATTAAGAAGAAGAGCCACT
GATTA AAAAGCCAGCTTCCGATGAGTCAGAATCTATGGATATAGCTAACTCT
GAAAGTGGAATGATTCCGATTCAAGTGAAGCTGATCCTAGGACGATACCAT
CTTTCTCTATACCTCTTCCCGACACACCACCTCCAAATTTTGCGAAAAGAGGA
GAAATACATGTAGATGTAGATCAGAAAAATTCCAAGCAATCAGGAGAATCAC
AATCGCCTTGGGAGCGGTAAGAATATTTATCCTAGCCAGGTGTTATAACAAA
ATTGAATAGTTTCAGAGCAAGAGAAAAGTCTGCATCGAACCCATTGTCCTCT
CCAACAATGAGCCGACCCAGGATACACTTCCTTCATCCAGCATATCAAAGTTT
CACAAATGATTCAGTTTCACCTCTACCACCACCGCCACCAGAGCCGGCTCCA
GCTCGTGAAAAAGTGGAATGAGTGGTGGTCCAACCTACTTTCAAATGACTTTCA
AAAAAGCTGCAAATATTCCTATCTTGAAGACATCGGCATTTGAACAACCATC
ATCACCTCCACCTTCCTCATCAGTTTCTTCATCAATTTCAATTATCTGAAGTGAA
TTCTTCTACATCGATAGCCTCCGAGTCTTCTCCAGCGAAAAGAAGCTCAAATT
TCGATTTAACTGCCTCAAATGAGCTTCCACCACCTCAGATGGTTGAACTTCCC
AAGCTCTCATTTTTTCAATATGCCTCCAGCCGTTTCGCTCCGCAGAGGTTAGTTA
ACTTTTTCCCGGTTTCATGAAATTTAGCGGTATCTGTCCTCCTTTTGGTGTGT
GCCCTCACAACCTAACCTCTTTTATCCAGGACGATTCTGCGATGACGTCGGAA
GAACCGATCCTTCTCCTCCGTTCTCCGAATTCCGCCACTCCTGATGATGATGC
ACTTTTCTCAGACCCACCCACCCCAAGATGACCGAATCAGAAATTCAA
GCACTGGTGAGCCAGATCACACATTTTCGATGTCGTGTGTGGAACCCAGGAAT
TTCAGACCGTTTTTTCTTTACACCTCATCCCCTTTTGTGTTATGTTAACATTAT
TTTGTGTCTCAAACACTGCATGCTTTTGCACCTTGGAATTAATAAATAATGCG
TTCTGGGATTTTGTGTGTTAAGGTGGAGTAGAGTTTGTGAGGCTAGAAAGTAT
GCCTTTTTCGTTTCTCCACTGCAAAATTTTCGTTTGAAAAAACAAAAAATTTA
CTAAAATTTGAAATTTACCAACTTGCCGTTGTCACAGCTGCTGAAATACAGT

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FIGURE 23

TTTTATTGCATTTTCACCCTTTATTGCATATTATTATTAGACACCTTTTAGGTC
AATAGGCAACCGAAAATATCCGAATTTGACTTAAAATGTACCTAAATTAAGG
AACTAACTTGAGATATACGACTAAAAATGCAATAAATTGTGAGAATTATTGT
TATGAAATTCAGCCGTTTTAGGCTAGTTTTAGCCAAAAACCGACAACTCTAT
TCCAATTAATTTTCCACTCCTGCACCTCGATTAGTGATTTTTTTGAAGAAAAAA
AATTATCTTCTTATTTTCAGAAAGTAGCGACGGAAAAAGTGAATCAAGTAATT
GCTCGACGTGAAGATTCTGAAAAAGATGTACGTCACAGAGAAGATCGAGATG
ATTATGATAGACGACGTGACGACCGTGACAGAAGATCCAGAAAGACTGATTC
GGAACGAAATGATCAAAGAGGACGACAACGTGAAGATGATGAACGAAGAGC
TCGAGAACGAGAAAGAGAAGTTACGAAACGACATGATCGGGAAAGGGAAGA
GATGCGATTACAGAAACAAAAAGATGAGGAAAGAAGAAAGAAAGATGAAG
AGGAAAGGATACAAAAAGAGAATGATGAGAAAAAACAAAAAGAGGATGAA
GCCAAAATGGAGGAGGAGAAAAAGAAGATTAAGAGGAGGAAATGAAGAT
TCCTGAATTTGAGTTGATTAGCGAATCAAATATTTGACGAGGAATGCGAAT
AAAAAGAAGACTGAATCCTTAACGTAAGTTATTATTTATAAATTTGACTTAAA
AATTGATAACTTTCAAATTAAGTGATTCAATAGACTCAAAGAATGAAAAA
CTAGAGTGCGCCTTTAAAGAGTACTGTAATTTCAAACCTTTTGTTGCTGCTCAT
TTTTCATCGATTTTTCTTAGTTTTTCGTTAAAAATAATTCAACCATTGGATTAA
AAAAAATTAAAAACACATAAATTTTATTTTGAAAAGTAATGAGAAAAACTAT
AGAAATTCGCCGAAAATTCTACAGCAACAAAAGCTCAAATTTACAGTACTTT
TTAAAGGAGCACATCTTTCTGAATTTAACAAAAATTCGGAGATTTTTCTTTTT
TTCGTGTTTTCTGGCGAAAAAACGATTTTTTCGCTTTTACCGGAAACGGTATC
CGGAGGAAAAAAGAACGAAAAAAGCGAAAAATTTTAAGAAGTTTCAAGAT
TAGTTACAACTCTTTTCAAAGCAGATTCTACAGTTTTTTGGGGTTTTGCCA
AAAAATTTATGAAATATAATGTTTTTTAGACTAGAAAAATAAACTAATTTTAA
TTTTCAATCAAAGCTCATTATTATATTTATATTTATATAATTCAGTTGCGAAT
GCCATCGAACTGGTGGAACCTGTTTCGGACAATACTTGTGTGAATCGTGCAAT
GCTCACCGAGTGCCCATCATCATGTCAGGTCAAATGCAAGAATCAACGATTT
GCAAAGAAAAAGTACGCGGCTGTTGAAGCATTCCACACTGGAACCGCCAAA
GGATGTGGACTTCGAGCAGTGAAAGACATAAAAAAAGGAAGATTCATCATTG
AATATATAGGAGAAGTTGTGGAAAGAGATGATTATGAGAAGAGAAAAACGA
AATATGCAGCTGATAAAAAAGCACAAACATCATTATCTCTGTGATACTGGAGT
CTACACGATCGACGCAACAGTCTACGGAAATCCATCTCGATTTGTGAATCAT
AGTTGTGATCCTAATGCTATATGTGAGAAATGGTCTGTACCAAGAACTCCTGG
AGACGTTAATCGAGTTGGTTTTCTTCTCGAAACGATTCATTAAAGCCGGCGAA
GAAATCACATTTGATTATCAATTTGTCAACTACGGACGTGACGCTCAACAATG
TTTCTGTGGAAGTGCTTCATGTAGTGGATGGATTGGGCAGAAACCGGAAGAA
TTTTCATCTGATGAGGATGATGATATTGTGACTACAAGGCATATTAATATGGA
TGAAGAAGAAGAAGAAAAAGTTGGAAGGTCTTGATCATCTTGGAATCATGAA
CGGAATGAAGTGATCAAGGATATGTTGGATGATTGGTCAATTCGGAATAAGA
AGCATGCTAGGAAGGTTATCACAATTGCGGTAAGCATTATTTGTAGAGAAA
ATTTAAAAATTAAAGATGGAGTACCGAAATCCGAGAAATATATTTAATTGAC
TCCAATTTTCTCTGATTCCGAATTTTAAATGAAAAAATTCAAAAAATTT
CCTTGATTTTATGTTTTAACTTGAAATTGCGAATTTCAATTTGTACAGATTTTTG
AAACGCCGAATTTTCGCGCCAGAGAAGCCATGTGTCGATTTTTTGAGATTTGTG
TATATTTACAAGATTTTGAATCTTCATCGGATGCTGATTTGCGTTTTTTCATCAT
TATATTATCAAAAAACTAACAATTTGTTTCGGTTTTACGGAAATTAACAATATA
GACTAGACATTTTCGTAAATATACACAAATCTCGTAAATCGACACATGGCGTC

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FIGURE 23

TCTGGCGCGAAAATTCGGCATTGAAAAATCTTATGCGGGCACTAATGAAAT
TCGTGATTTCAAGCTGAAATATAAAATCAGGGAATTTTCCTTGCATTTTTTCA
CTCAGAACTTCGGAATCAGTTGCAAATTTGGAGTCATTTGAAAATATTTCTCA
GATTTCCGGTACTCCACCTTTATTATAATTTTTTAAAATTTTTTAAATGATTTTTT
TTCCATGTTCAACAAAAAATAAATTTTCAGTCTGCAATGACCGATTACTCTC
AACGTGTGGATGTCATTCAAGAAATCTTCTCCTCAGACACCTCCGTAACCGTT
CAAAAATTCTATGCAAAAGAGGGAATGGCTACATTGATGGCTGAATGGTTGT
CTGAAGATGATTATTCGCTGGATAATCTGAAACTTGTTCAGCTATTCTCAAA
GCTCTTCACACTGAACTATTCGATTCTGTCGCCAAAAATGATCGACTCTTACG
AGATTCTACATCACGATGGGTCAATGCGAAAAATGGATGAATATGTTGATATA
CAAGTGATAGCTGATTCACCTATTGCTTGTGTTGAAGATCCCGTACAGGAGTA
CAAGGATGTTTGCAAAGTTATAGAGGTATATACATATTAATTTTTTAAAAAAG
AATATTTTTTGCATGTCACAAAATATTTGGAAATTTTCCCGAAAAACCCATGA
AATCAAAAAACAAATTAATAGTAAAATTATTTCTCCTACGAACATTTTTTCG
ATTTTTTCGTTTTCCGATATTCCTTTTTAAAAATCTGATTTAAAAAATAAACT
TAAATTTTAGGTCTTTTTGCTCCTTTTTAGAAGCAATTTATATGTTTTTTAAAA
CAAACTTAAAATTAGCATTTTTATGGGTAATTTCTGAACACATTTTTTTTTTC
GAAAAAATGGCCAGAATTTCAACCACTTCTCCGTAAAATCGAAATTAATA
ATTTTTTCTCTATACATTTTTCAAAAAAAGACTCCTCATTTATTGTATTAGATA
CAAATATATGTTTTCTCATCAAAATTTACGAAATTTGTTATAATTTTGAATTT
TTTTTGTTTTTTTTTCGAAAAATTGAAAATTTTCTAATTTTGAAACGATATTAT
ACAATTTTCAGCGCCATCAATTTAACTAATTAATAATTTTCAGAAAGGTCTCGT
CGAAAACCTTCACAAGAGCCAAAGAGATGGCCTATCGGTTAAATCAATACTGG
TTCAATCGATCAGTGAGCTTCAAAATTCAAAAAAGATACGTGATCCTGTGC
CAAAAGATGTTCCAGTCAGACAAGAAGATGCTACAACATCATCACAATCTCA
TGATAATAGTAGTAGAACTGTATCACCGAATCATCGACATCATTATCTTCAT
ATTCAAATTCATGTTATCAAGAACGAGAACCATCTCATATACGATTCTTTAAT
AATGGAAATGATGTTTCATCAATATCGTTTTGGAGGTTATCATGGAAATACTA
CAATGATAACTATTTTCAGTAGAAGGCCCAATAAAGGATTCATATCGAGATCGC
CGTCGATTTAATGGACGTGTTTCGAGAAGTCGATCAAGAAGTGTCTCACCAC
AGAACTATAAAAGAAGAAAACCTCGATGAACATGACAATAATCATCGTCAGC
GTTCTCCAATTCGTGATCGTCACACATCTCCCGGCGGCGAAAAGACTCCTAGC
TCGAATAATTCTGGAGAACGAACTATAAAAGACTGGATATTCGAGGAGCTC
GTATAAAACTATAAAAGAAGATTTGGAAAGCTGCTGCTGCTGCTGCTGCTGC
TGCTGCTGTACCATCAGAAGTGCAAGCTTATCCTCATGAACATACAGCTGTAC
ATCAGAGTGTTTATCAGATGCCAGGTTATGAGTCTTATGGTTGGTTTAGTTTT
TTTAAAAATATCATTTACCAGGGTGCCATTTTTTAAAAATAAAAAATAACTCGGA
AAATATGTTTTTAAAAAATTTTCAGAATTTCTCTCATCAACATAAAACTTGATA
-AAAATCGAATTTTTATTATTTTCTAAACATTTTTTTCGGTTTTTCCGAAAATCAA
AAAAAAGTTTAGAAAATAGCAAAAAATCAGTTTATTAGAAATCAAATTTTG
TTCGTTTTGATAAGAAAAAACATAAGAAAAACATGTTATTTTCTTCTGAAAAA
GAAAAAATCGAAAAATCTATGGCCTTTTGGCAAAATGTTTTGGACCAAAAA
ACAAAACAAATAGCATTAAATATTAGTTCTTTTGTTTTCTTCTAAAGTTAA
TTTTCTGAAAGTCTTGCTTGTCTGATATCAAATAAAAAACATTTTTTCAGGAGTA
TATGATCCTGTAAATGGTGTCTACATGTATCCTCATCCTGGCGCTGGTTACTA
TCCACCTGCCTATCCACAACAACCGATTATGTTAACAATGGACACTCTTCCAC
CGAATGATCGTCTTGGTGAACTTTACGAGAAAGCCAGTATCGAGCAGCTAGC
GTGAGCATTTTTTAGTTTAAACCTTTCGGATTACCTAGAAAAATGTTACCTTT

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FIGURE 23

GACGCAAAATTACGGTAGCAGGTCTCGTCGCGACCGAAATTTTTTCAGCGGAG
TACGGTAGCTTCCCATGAATTTTTTTGCTGAACCTTATCTTTCTGATAACAAATA
GTAACATAAAACATGAAAAACTGAATAAAAAATTGATATCTTTACCTTATAGGC
TCTTTAAGGGCGCAGACACAAAACTGACCGGCTACCGTAATTTTTTCGTCAA
AAGTCACACATTTCTCAACTGGTGAAATCCGAAAAAATTGAAATTTTTACTAC
TCGTCCGACTGTTTAGAAAAAGATTAAAAAAGAAAAAAGAATGTCGGTT
TTTCGAATTTTCGATTTTCAAAGAAAAAATCAATATTTAAAAATCATTTCG
GTAATTTCCCTAAATTTGTAAAATATAATTTCCAATAAATGTTTTTTGTTTTCC
GGAATTTTAATAAAAAATCAATTTTCGCGTAACAAAAATGCGAAAAAATGAC
TAGCCACTCGAATATAATAACACATGAAATAAAATTAAAAATTATTACAGTCA
ACGAGATGCAATTGTGAGACAAGAACTTGAGCTGATACGTATTCAAATCGAA
AGAAAAACTGCTCAAAAAGAAGCGATCAAGGCCGCTTGCCGTCGTGCTAACG
AAGAAGAAGCTAAACGACAAGAGGCACTTGCAAAGACGAAATATGTTTGGG
CGATTGCAAAGTCAGAAGCTGGAGAGACGTATTACTACAACAAAATAACAA
AAGAGACGCAGTGGACAGCACCAACACCAGTTCAAGGTCTTCTCGAACCGGC
TTGTGGTGCATCTCCTGATACTACAGTTGTCATTGCTGACGAGATTACTGAAG
AAGAGCAACAAGCTGAAGTTCTGGAGAAGCCGCGTGTTGTTAAGGAAGAAG
TTATCGAGCCAGGTTCACAATCTGAAACTCAAAAAGAATCTCCGGAGAAAGT
TCGAGTTGTTGTACCGAAAGTTGAAGTTGAAAGATCACCGTCGCCAAAATCT
TCTCGTGATCGTGAGAAGGATCGAGAGAAATCTCGTGAGAAAGATCGTGAAA
GAGATCGTGACAGAAGAGAAGGTTCAAAACATCGTGATAGTTATCATGGACA
TCGAAACGGCAGCAGTTCTGTCACTGAACGACGTATGCGAGAGTTCAAACAT
GAGCTGGAACGATCCACTCGATCTGCCGTTCTGTTCTCGTCTACAACATCAACG
TGACGCTTCTAGTGATAAGACTACTTGCTTATTAAGTTAATATATCGAGAGA
TTTTCAAACGAGAAAGTGCGCAGAGTGGATTTGATTATCGATTCAGTGAGAA
TACTGATAAGAAGGTAATATTATGGACCAAAAAATAAACAATTGAAAAAAA
AACCAAAAAAATCTGATGCTTGAATTTAAAAAACAATGAAAGAGTGCA
ATTTTTTAGGTTTTTTGGTCTTTTTTTTTTGAAAAACCAAAAAATAAATTTTT
TCCAAAGTACCAAACTTCATTTTAAAAAATTTATTTGACATAAAAATTGATA
ATTTAAACTAATTTGAACATTTTTCCGCAAAAATTATAGATTTTTCTGCCAA
TTTTAGATTTTAAACGTTTTTTTTCGGACAATTAATGTTTCGAATCATCAATCA
GAATGAATATGATATCTGATGAAATTCAAAAATAATGCAATTTAAATAGAAA
ACGGTACAAAAGTTTTGAAAAATTTAGAAGAATTCTAAAAAATCCTGTCC
TTCAGGACAAAATTCAACCTTTTTCTCAAAACACAAAAATTACTTTATATTAT
TTTTCAGGTGAAAAACTACGTCAAGTCATATATCGACCGAAAACTCGAATCA
AACGATCTCTGGAAAGAATACTCTCGGCCATGAGCTTTATTTTTTAATTTAAA
TTTTATAAAAAAATGTTTATGCTTGTTTTTTTTCTCTATAGTTCCCTCCTATCCC
CCCCCTCCCCTATCGCCTAAAAAATTGATCTCTGTCTGATTTACCGATTTCGGT
TTTATTTGATCCCATTTGAACGAGTATATCATCATGTTCTGAACTTCAACGTT
GCACATTTTATTCCCCTAGTTTTATGTCCCCAGAATTGTTTTATACTATCCTGT
AATCCACCTCAAAATGACAGCCATGAAAAGCTGTTTTTTCATGTTTTCTATTTT
CTTGTTGATCGTATTTGCGCGCGTCTTTGTCGCGCAATTTTTTTTGTAATTAA
AAAATGAATTACGGATGTTGAATTTTTAAATTTATTTTTTTAAAGAAAAATTG
TGGAAGTTTTTCAGATTCTATACTGCTTATTTTTACGCTAAATTTTTTTTCGAA
GTCCCCTTTTTTCAAATCGAAGTGTAAGTGCCTCCACGATCAATAGAGACTC
TCCGCCCTCGAACCATGGGTCTCGTTAGGTATTTGGCAGACTTACCGTAAATT
CAAATGTTTTATTACTTCGCGACTAATTTTTTTTATTCATGACTCAATTTTTTAT
CAATTCCAACGAAAACTAATTA AAAACAACGGAAAAACATAACGAAAAATG

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE LET-60 RAS SIGNALING
Applicant(s): Horvitz et al.
Filing Date: September 12, 2003 Serial No.: N/A
Page 72 of 91 Customer No.: 21559

FIGURE 23

CTTGAAAATTGCAGACATTTCCGAAATTAATTAAATTCCTAACGAGACCCATG
GCTCGGGGGCGGAGTGTTTTTCGATTAGCCATGGAGCGCGTTGAGATATTCCT
AAATTTTTTCTATTCAGATGTCGAATCAATCAAAACGGGTCACAGTGAGAATT
GAGCATTCTGAAGAACAACACTTTTTTCGAAAAGTAATTTTCAAATTTTGATCCAAA
GAAATTATTCGTCAATTTTCAGAGTTTTTAAAATTCCAACATCAAGAGCAAGA
AGATCGGAAGCTCAAATATGTTCTGCACAAAGCTCACGAGAATCTGAGAAAG
TGCCCATTCGAGATTCTGACAATTG

Figure 24 LIN(n3628) Protein

MFQRKVVLPPKRTMVQTRRKTAQAVQDGGAVKENKAKPPAPQTPTKRAKRG
RPPKIKTDANTLNTPTSSNLVDDKLLIESESQDSILTNEADSFLEKEVEEIEDSSDI
LPDKINSPEKPSVLVKRRSSTRLKVKTDEDEKDVVNIEVAVLEEKSIQIEPTSPA
PEDPQPSTSSLPLVEPIEDIVEPNEPTSSADPPVSNIKDEDIKEEEPLIKKPASDESES
MDIANSESGNDSSEADPRTIPFSIPLDTPPPNFAKRGEIHVDVDQKNSKQSGE
SQSPWERAREKSASNPLSSPTMSRPRIHFLHPAYQSFTNDSVSPLPPPPPEPAPARE
KVENGGPSTTFKMTFKKAANIPILKTSAFEQSSPPSSSVSSSISLSEVNSSTSIASES
SPAKRSSNFDLTASNELPPPQMVELPKLSFFNMPPAVRSAEDDSAMTSEEPILLR
SPNSATPDDDALFLTTPPPPKMTESEIQALKVATEKVNQVIARREDSEKDVRHRE
DRDDYDRRRDRDRRSRKTDSENRDQGRQREDDERRAREREREVTKRHDRER
EEMRLQKQKDEERRKKDEEERIQKENDEKKQKEDEAKMEEEEKKKIKEEEMKIPE
FELISESKYLTRNANKKKTESLTCECHRTGGNCSDNCTVNRAMLTECPSSCQVKC
KNQRFKKKYAAVEAFHTGTAKGCGLRAVKDIKKGRFIEYIGEYVERDDYEKR
KTKYAADKKHKKHHYLCDTGVYTIDATVYGNPSRFVNHSCDPNAICEKWSVPRT
PGDVNRVGGFSKRFIKAGEEITFDYQFVNYGRDAQQCFCGSASCSGWIGQKPEEF
SSDEDDDDIVTTRHINMDEEEEEKLEGLDHLGNHERNEVIKDMMLDDLVRNKKHA
RKVITIASAMTDYSQRVDVIEQIFSSDTSVTVQKFYAKEGMATLMAEWLSEDDY
SLDNLKLVQAILKALHTELFDSKANDRLLRDSTSRWVNAKMDEYVDIQVIADS
LIACVEDPVQEYKDVCKVIEKGLVENFTRAKEMAYRLNQYWFNRSVSFKIPKKI
RDPVPKDVPRQEDATTSSQSHDNSSRTVSPNHRHHSSSYNSCYQEREPSHIRFF
NNGNDVHQYRFGGYHGNNYNDNYFSRRPNKDSYRDRRRFNGRRSRSRSRVSP
QNYKRRKLDEHDNNHRQRSPIDRHTSPGGEKTPSSNNSGERNYKRLDIRGARIK
TIKEDLEAAAAAAAAAAVPSVQAYPHEHTAVHQSVMQPGYESYGVYDPVNG
VYMYPHPGAGYYPAYPQQPIMLTMDTLPPNDRLGELYEKASIEQLAQRDIVR
QELELIRIQIERKTAQKEAIIAACRRANEEEAQRQEALAKTKYVWAIKSEAGET
YYYNKITKETQWTAPTPVQGLLEPACGASPDTTVVIADIEETEEEQQAELVKPRV
VKEEVIEPGSQSETQKESPEKVRVVVPKVEEVERSPSPKSSRDREKDREKSREKDR
ERDRDRREGSKHRDSYHGHRNGSSSVSERRMREFKHLELSTRSAVRSRLQHQ
DASSDKTTWLKLIYREIFKRESAQSGFDYRFSENTDKKVKNYVKSVIDRKLESN
DLWKEYSRP

Figure 25

lin(n4256) genomic sequence (1 kb of upstream and downstream genomic sequence is included in this file).

<u>Exon number</u>	<u>Exon boundaries (inclusive)</u>
1	1001 – 1096
2	1166– 1453
3	1501 – 2199
4	2298 – 2730
5	3234 – 3847
6	4148 – 5778
7	6111 – 6333

GCTTGCATCGAAACTCTTCTCATTATTTACGTGATGATCACATCTTTCGTTGGG
 CTGTA CTCCCTCCGGTTCTTCGTTCTCTTCGACCTGTTCGAAAAGATACTCCA
 ATGCCAACGATAATTATTAATTCTTCAATAGTTCTTGTTGTTGCATCCGCTCTC
 CCAGTAGCTGTAAACACAGTTGGAATGACAACCTTTTGATCTTCTCGGCTCCCA
 CTCATCGCTCCAATGGCTTGGATCATTTTCGAGTCGTTGTTGCCTATAATACTCT
 ATTCGTCGTGTTGTCTGTCGCATTTCTCTTCAATCAATTGACTGCTTCAATGAG
 AAGGCAAATCTGGAAGTGGTAAGCTGTGCAATTTAAAGTTTAAATTCTTATTA
 ATTTTTTGCAGGATATGTCAACTACGATGTGGAATCAGACGGGAGAGTGAT
 GCGGATGAAACCATTGAGATCCTTAGAGGCGATAAGAAAAGCAATTGAATTT
 CTTTCCTTTTTCAACACTTCTTACCCATGTTTCATCATTTTAATCTTTTCATTACA
 AAAACAAGGTCCTATTTTTTTTCTCGGGTACTACTCGCCTTTTCTAATAATTCA
 GAATCATCAATTTTTGCCAACCTCTAGCTTTACATGTCTGTTTTTCATCATTTT
 CTCTCAAGCATTCTCCTAATATATTATGTTCCCTAGTATTTCCCTCAGTCAGC
 AATTTTCTCGTCGTCGAAACCGTTTAGCTTTACTTTCAATCAAAACGTGGAAC
 ATTTTTCAAACCTATTTGAAGCCAAAAAAACCAGGGCTTTTGTATATGTACCA
 TATTTTCCCTCTGATTTTCTTTATCGCCTTCTCTTTTCATGTAGAATAACTGAA
 ATACAAACCATTTTAATTTTTTCTTTAATTATCAATACTGTCCGTATAGGTAA
 AAATTATTTCTTCAGGTTTGAAAAAATCCGAAATATGTATCTGCAACTCTTCA
 GGGCATTGCCTCAATTAATTTTTATCTAATATTCAGATGGACCAACAAGAACC
 ATCGAATAACGTAGATACGAGCAGTATTCTTTCGGATGATGGGATGGAAACA
 CAGGAACAAAGTTCATTTCGTCACTGCTGTGAGTGAAATTATTTAAAATTTTCGC
 TTCGGAGATTTCATTGTCATATAATTCAATTTATCGATTTTCAGACAATTGACC
 TAACAGTGGACGACTACGATGAAACAGAAATACAGGAGATTCTGGATAATG
 GAAAAGCAGAAGAAGGAACAGATGAAGATTCTGATTTAGTTGAAGGGATTCT
 TAACGCTAATTCAGATGTCCAAGCGCTCCTTGATGCGCCATCTGAGCAAGTA
 GCTCAAGCTCTTAATTCGTTCTTCGGAAATGAGAGTGAACAAGAAGCTGTTG
 CAGCACAAAGACGGGTTGATGCGGAGAAGACTGCCAAAGATGAAGCTGAAC
 TCAAGCAACAGGAAGAGGCGGTTAGATTGCAATAAAGGAAACAATAATAAA
 ATTATTTTATTTTCAGGAAGATCTTATTATAGAAGATTTCGATAGTCAAAACTG
 ATGAAGAAAAACAAGCAGTTCGAAGACTGAAAATCAACGAATTTTTATCGTG
 GTTCACAAGGCTCCTTCCAGAACAATTTAAAAATTTTCGAATTCACAAATCCGA
 ACTATCTGACAGAATCTATCAGCGATTACCGGTTGTAAATGTGATAAATGC
 AAGGAAATTGTCAAATCGTTCAAGGAAAGTGAATCACTTGAGGGACTTTCAC
 AGAAATACGAATTAATTGATGAAGACGTGCTAGTCGCTGCTATTTGTATTGGC

FIGURE 25

GTTCTCGATACCAACAACGAAGAAGATGTCGACTTTAATGTTCTATGTGATGA
TCGTATCGACGATTGGAGTATAGAAAAATGTGTCACTTTTCTTGATTATCCAA
ATACTGGATTGAATTCGAAAAATGGACCGTTGAGATTCATGCAGTTTACTGTC
ACATCACCTGCATCAGCAATTCTCATGCTCACTCTGATTTCGATTACGCGAAGA
AGGGCATCCGTGTCGATTAGATTTTGATTCAAATCCGACTGATGATTTACTCT
TGAATTTTCGATCAAGTGGAATTTTCTAATAATATCATTGATACGGCAGTCAAA
TACTGGGATGATCAGAAGGAAAACGGTGCGCAGGATAAAAATTGGCAGGCGA
GTATTAATCAAACCTCACAACCTGTTTTGAAAGTATTTTCATAATTATCACTTAA
ATACCTTTTAGAGAGCTCAACGACTTCTTCCACGAAATCGAGTCAACATCAGC
AGAATTCAAACAACATTTTGAGAACGCCGTGGCAGCCGTAATGAAATAATT
CAACTTGTCAACGAGAAAAATCCCGATTTTGATGGCACTGAGGCTGCTGTGA
ATGAGAGTTTTACATCCGATCAACGAACCGAAATTATCAACTCTCGTGCAAT
AATGGAGACATTAAGGCCGAGATGAAGCTCGCCATCGCCGAAGCTCAGAA
AGTTTACGACACCAAGACTGACTTCGAAAAATTTCTCGTTTTGACAGTTGGAG
ATTTCTGTCTGGCTCGCGCCAATCCTTCTGACGATGCAGAATTAACATACGCC
ATAGTTCAGGATCGTGTGGATGCAATGACCTATAAGGTTAAATTTATCGACA
CAAGTCAGATCAGAGAGTGTAACATCAGAGATTTAGCCATGACTACGCAGGG
AATGTATGACCCGAGTTTGAATACATTTGGTGATGTTGGTGAGTTTAAAGTTA
AAATTGATATTTAATATTACATCTGTTATGTAGAATAAGGGTTTCGGTTTTTC
GATTTTATTAGAAAAATCGAAAAATTTAGTTTTTGTGTTAAATTTAAAAAATC
AAAATTTGATTCATCTATCAAGTCCGTTTTTCTCTTCTCAAATTTGACAAAATTT
TGATAATCTAGAATTTTCGTCCCGTATATTTTTCAACGAAAAACCATTTAAAA
TTTTCCATGATTGGATTTTCGGTTGATCTAGAAAAAATGGTGCTAAACACTA
AATTTGAAAAAGTTTGAAACAAATTCAAATCCAAATATTTTCATGAAAACTT
GTAAAATATATTATGTACACAAAAAACGTTTCAAGTGTAGCAGTTGTTTTT
GTGGTCCCAAAAAAGCAGATGTTTGTGAGAATCCATTAAACAACAAAAAAT
CCAAAACTCAACCTGGCCTAGATATCAGTTTCATGATCGAAGTATCTAAAA
TCATTGTTTTCAGGTCTTCGAGTTGCCTGTGCGCAAGTTATTTCTCGAGCCAA
TTTGGAAAAAAACAATTTGGCTTACCGGTACAGCTGCCGGACGTCGCAGAG
CTCATAGATCCGATTTTCTAATTTTCTTCGACAACGGAACCGATGCATACGTG
TCAGCTCCGACAATGCCTGGTGAACCAGGTTATGAAGTTGCTTCTGAAAAGA
AAAGTGTATTTTCTCTCAAAGAAATGATTGCGAAGATGAATGCTGCTCAGATT
GCTATTATGGTTGGACAGCCAGTAGGAAAGGAAGGAATCTGGATTATTTTT
TGACATTTTCATTGGATTTCGACAATCTCACAGATCAGCGTATATTCGGGATTTT
ATGAAAGAATTTCCGGAATGGCCACTTCTCAAGATGCCAGTTGGAATGCGAA
TCTGTTTGTACAATTCTTGTGATCGACGTAAGAAAAATGGTGACAGTGATT
GGAAGTATCGAGCTTTTGCTATTGTGAGACACGAAGCACCGAATCCATTGG
CTCCTGGGAATAGATGTACAGACTTTCCGTGCAATGATAGAAATCATCAGCA
TATTGACGAGAAAAATCTATAGAGGATCTCATAGATTGGAAGGCGCAGCGGTA
AGATTTTATTTGAAAAATTGATACAAAACGAGGATTTTCTAAAATTATTTTAT
TTTTATTTGATTTGATTTCTTATAATTGATAATCAAGGTTTTTTGGATGTTTTG
TTAGAGAAATCGAAAAGGGAACTTCCAAAAAAGCTGTGAAATCAATTTT
TGCTTTTAATAATATCCAAGTTTCATCTTCAAAGTTTTTTCTATAAAATGGACA
CAAACTTTCAACGTTTTCAAAAAAAGGTTCCGAAAATATGAAAAAAGGAG
AAAGAAATCATGAAAATTTTGATTATTTTCAGCACAAAGAAGCACATGATCTC
GACAAATAACAATCTGTGCAACGCAGAAAAGACCAGCTTCAATCACAGTTC
GAGCCAACCGACATGATTCGTTTCGATGCCAGAGAGGAATCACCAACAAGTCG
TTAAAAAGAAAACGACGGGCACCAATCAGAATGTCGCTTCGACAAATGATGC

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING

Applicant(s): Horvitz *et al.*

Filing Date: September 12, 2003 Serial No.: N/A

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Customer No.: 21559

FIGURE 25

AAAATCGAAGAGAGAAATTGAAATAAGAAAGAAAAATCAATTCTTATTTAAC
AAGATTATTGTTCCAATACCCGTCCTAACACCATTGGAAAATCTCAAGGCTCA
TGCTCAATGTGGTCCAGATTGTCTACAGAAAATGGATGCGGATCCGTATGAA
GCAAGATTCCATCGAAATTCACCAATACATACTCCTCTTTTGTGTGGTTGGAG
ACGAATTATGTACACAATGAGTACTGGAAAGAAGCGGGGAGCAGTGAAGAA
AAACATTATTTACTTTTCTCCATGCGGAGCCGCTCTTCACCAGATCAGCGACG
TCTCTGAATATATTCATGTACCCAGAAGTTTATTGACGATTGATTGTTTTTCAT
TTGATGCACGAATCGATACTGCCACTTATATTACTGTTGACGATAAATATTTG
AAGGTTGCTGATTTTTCGCTTGGAACCGAAGGAATCCCAATTCCACTAGTGAA
CAGCGTGGATAACGATGAGCCTCCATCATTGGAATATTCGAAACGACGATT
CAATACAATGATCAAGTGGATATATCGAGTGTTAGCCGAGATTTCTGTTCTGG
ATGCTCTTGTGATGGTGATTGCAGTGACGCATCGAAGTGTGAATGCCAACAA
TTGTCCATTGAAGCAATGAAACGACTCCCCCATAATTTACAATTCGACGGAC
ACGACGAATTGTATGAGAGTTCAGAAAAACAAAATAAATTTTTAAAACATTT
TTTTTTCAGAGTTCCTCACTATCAAAATCGTCTTCTCAGCAGTAAGGTTATCA
GTGGACTCTATGAATGCAACGATCAGTGTTTCATGCCATCGAAAGTCTTGTTAC
AACAGAGTTGTTTCAGAACAAATATCAAGTATCCTATGCATGTGAGTTTATTTAA
CGATGATACATAACCAATTATTGTTTTTTCTTCAGATCTTCAAACCTGCTCAATC
CGGATGGGGAGTCCGAGCTTTGACGGATATTCTCCTCAAAGTACGTTCAATTTGCA
CGTATGTAGGTGCTATACTGACGGATGATTTGGCTGATGAACTAAGAAATGC
GGATCAATACTTCGCTGATTTGGACTTGAAGGATACCGTGGAGCTGGAAAAG
GGTCGCGAAGATCATGAAACTGATTTTGGTTACGGAGGAGACGAGTCAGATT
ATGATGACGAAGAAGGAAGTGATGGTGACTCCGGTGATGATGTAATGAACA
AAATGGTGAAACGTCAAGACTCTTCGGAGAGTGGTGAAGAAACAAAACGGC
TGACAAGACAGAAAAGAAAGCAATCTAAAAAATCCGGTAAAGGAGGAAGTG
TGGAGAAAGATGACACCACTCCAAGAGATTCAATGGAAAAGGATAATATTG
AAAGTAAAGACGAACCCGTTTTCAATTGGGATAAGTATTTTGAGCCGTTTCCA
TTGTATGTTATAGATGCAAAACAGAGAGGAAATCTTGGAAGGTAAGATCACA
ATTTTATTCATTAAAAAAATTTTTTAGAGATTTTGCTTTAAATGATAAAAAAT
GGACAAACCAACCGTTTTGCCTCTTCTTTTGGTTTATCAACCTTTCTCTATGGAA
AAAATTCTGAAAAATTAACAAACAGTATTTACGTTGAAAAGTGAAGAAAAA
AGCAAAAAAAGGAAACAAATTTCAAACCGTTCTACTCCATCTTAAAAAAAC
TAAATTCGTAAAAAGTCATTTGGTATGTTTTGGAGACTATAATACAATTGAG
AAAATTTGAAAAACCGGCACTCCAAAGATACAATCATAAATTTTCGATAACT
TTCAGATTCTTGAATCACTCTTGCGATCCGAATGTGCACGTTCAACACGTCAT
GTACGATACGCATGATCTTCGTCTTCCATGGGTGCGGTTTTTCACACGAAAAT
ACGTGAAAGCCGGCGATGAGCTAACCTGGGACTATCAATATACTCAAGATCA
GACGGCTACCACACAACCTCACATGCCACTGCGGAGCTGAAAACCTGCACCGGC
CGTTTGCTGAAAAGTTAAAGAATTGTTGTTATTTCTTCCCAGTTATGTTTTCC
TTTTTTTTTAAGTATTTATTTATTTAATTTTTATTTGTTTATTGTTCAATC
GTTTAAATCTCCCTTTGAAAACAGCATCTCATATGTATGATCTAAACACGTA
TTTACCTCGTAAGGGTTTGCCAAATAGTTTCTTTGGTTTTTCAATTTGATTTTCT
CTGCGAATAAAATGTTTTAAAAAAGACATTATTTTTTAATAGTCAGTACAG
TTTTGATGTCTCCAATCTATTTTCAAGTTTACAATTTTAAATATAGAATATATAT
ATTTAGGTTTTCATAAGTTATGCATCGATTACGGGTTCTACGTCACTTGAAGTT
CTGCATTTCCACGTCACATAGGACTACTGTAGTTTTTAAAAAATACTCGTTTCA
TTTGAATAATATTCCTTCTACTAGTTTTGCTTCTGGTAATAATCGAATTTCAA
AACTTTAGCTAAAATATTTCTTTTTGAAGAGGCTGCAGCAAAATATGAAAAG

FIGURE 25

AAAAGTCCAACTGAACATGTATTACTTCGACCCGATACATATATTGGAGGTG
TCGCCATGCGAGAAGATCAAATTATTTGGCTCAGAGACTCAGAAAATAGAAA
AATGATTGCAAAAGAAGTCACTTATCCACCTGGATTATTGAAGATTTTCGATG
AGATTCTAGTGAATGCGGCTGATAATAAAGCAAGAGATTCCAGTATGAATCG
GTTGGAAGTATGGTTAGATAGGTAAATATATTGCAGGAATTTATGTTCTGCGA
CAAAGCTACGATACGCTGTCTCGCCACGACAATTGTTTTGGTAAATGCATGA
AAATCGACGTGCACCTTTAAATAATACTGTAGTTTTAAATTCTCGTTTCTTCA
ATTTTTCATAAAATGGTTTTCCGATGAATATATGATTTTAAAAAATCTAAAAT
TCACATTAATTTATAAGAAACAAAATTCCTCAAAAACGAAAGTTTGGCGATA
CAGTACTATC

Figure 26

LIN(n4256) amino acid sequence

MDQQEPSNNVDTSSILSDDGMETQEQQSSFVTATIDLTVDDYDETEIQEILDNGKA
EEGTDEDSDLVEGILNANSQVQALLDAPSEQVAQALNSFFGNESEQEAVAAQRR
VDAEKTAKDEAELKQQEEAEDLIEDSIVKTDEEKQAVRRLKINEFLSWFTRLLPE
QFKNFEFTNPNYLTESISDSPVVNVDKCKEIVKSFKESSEGLESLQKYELIDEDVL
VAAICIGVLDTNNEEDVDFNVLCDDRIDDWSIEKCVTFLDYPNTGLNSKNGPLRF
MQFTVTSPASAILMLTLIRLREEGHPCRLDFDSNPTDDLLLNFQVEFSNNIIDTA
VKYWDDQKENGGAQDKIGRRVLIKLTTVLKNAVGSRNEIIQLVNEKIPDFDGTEA
AVNESFTSDQRTEINSRAIMETLKAEMKLAIAEAQKVYDTKTDFEKKFFVLTVG
FCLARANPSDDAELTYAIVQDRVDAMTYKVKFIDTSQIRECNIRDLAMTTQGM
DPSLNTFGDVGLRVACRQVISSSQFGKKTWLTGTAAAGRRRAHRSDFLIFFDNGT
DAYVSAPTMPGEPGYEVASEKKSVMFLKEMIAKMNAQAIAIMVGQPVGKEGNL
DYFLTFHWIRQSHRSAYIRDFMKEFPEWPLLKMPVGMRICLYNSLVDRRKKMVT
VIGTDRAFAIVRHEAPNPLAPGNRCTDFPCNDRNHQHIDEKIYRGSHRLEGAAHK
KHMISTNNNLSQRRKDQLQSQFEPTDMIRSMPEPNHQQVVKKKTGTGNQNVAS
TNDAKSKREIEIRKKNQFLFNKIIVPIPVLTPLENLKAHAQCGPDCCLQKMDADPYE
ARFHRNSPIHTPLLCGWRIMYTMSTGKKRGAVKKNIYFSPCGAALHQISDVSE
YIHVTRSLLTIDCFSFDARIDTATYITVDDKYLKVADFSLGTEGIPIPLVNSVDNDE
PPSLEYSKRRFQYNDQVDISSVSRDFCSGCSCDGDSCDASKCECQQLSIEAMKRL
PHNLQFDGHDDELYESSEKQNKFLKLFFFRVPHYQNRLLSSKVISGLYECNDQCSC
HRKSCYNRVVQNNIKYPMHVSLENDTQYLLFFLQIFKTAQSGWGVRAITDIPQ
STFICTYVGAILTDDLADLRNADQYFADLDLKDTELEKGREHETDFGYGGD
ESDYDDEEGSDGSDGDDVMNKMVKRQDSSESGETKRLTRQKRKQSKKSGKG
GSVEKDDTTTPRDSMEKDNIESKDEPVFNWDKYFEPFLYVIDAKQRGNLGRFLN
HSCDPNVHVQHVMYDTHDLRLPWVAFFTRKYVKAGDELTDWDYQYTQDQTATT
QLTCHCGAENCTGRLLKS

Figure 27

lin-65 genomic sequence (1 kb of upstream and downstream genomic sequence is included in this file)

<u>Exon number</u>	<u>Exon boundaries (inclusive)</u>
1	1001 – 1133
2	4522 – 5208
3	6128 – 6361
4	7962 – 8350
5	8706 – 8928
6	9260 – 9516
7	10328 – 10567
8	11677 – 11700

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AAAAATTTAAAAAAATTTTAAAAAATTCGTGTAAAAATTACCCCGGTTGTTTA
GGAAATAATAAGAGATTAGAGACTTTTTTCAGATTTTATTTTCTTGAGTTT
TGCCGGTTTTTCAGCCGATTCTATCTTTTTTTCTCATTTTTTGAGTTTTTTT
CGCTAGTTTTCCCCTCAATTTCTCGATTTTTTCACGATTTTTTGAAAATTTTCG
GAAAATTGAATTGTTTGCAAAAAAAAAAATTCAAAAACCGCATTTTTCTCAG
AATTTTTCTGGGATTTTGTACAAATTTTGAATTATTTCTCAAAAAAAGCAG
GTTTTTACCGATTTTTTTGGTTTTTTCCCCAAAATTTTCCGATTTTTTCCGAGTT
TTGCCGGTTTTTCAGCCGAATTCTACTCTCGATTTTTTTACGATTTTTTGGAAT
TTTCGGAAAATTATTTGAAAAAAAAATCAAAAACCGCATTTTTTTTTTCTGAAT
TTTCTGGGATTTTGTACGAAATTTTGAAATTTTTCTCGAAAAAAGCAAGTTAT
TCCCCAAAATTTTCTGATTTTCCCCCAAAAATTTAGATTTTTTCCCGAGTTTTCC
CCAGTTCTCAGCTGATTTCTATATTTTTTTCTCAATTTTTGTGATTTTTTGTTGC
TAGTTTTCCCTTCAATTCCTCGAGTTTTTCACGATTTTTTGAGATTTCGAAA
AATTGTTTGAAAAAAATCAAGAAACCACATTTTCTCTGGATTTTCTCGAAAT
TTGCACAAAATTTTGAATTTTTTCGTAAAAAAAACGTTTTCCCCAAAAT
TTCAGATTTGTTTTTGATTTTTTTCGAGATTTTCCCCTGATTTCAAAGTTTTTC
CTGAATTTTTCGAATATTTCTGAAAAATCGGCTATTTCTAACTTTTTAAATAA
TTTTTTTTGAATTTCTGACTTTTTAAATCCTTTTTTTTTTGCCATTTTTTCCCATC
TAAAATTCTAAATTATTCAAAATTTTACAGAATGTCAGAAGTAATCGACGAA
AGTATCTTAAATACAGAAGCTTCAGATGATCCAATACCTCCATTAAATGATG
ATCAGATTGCTGAGCTTTTGGGTGAAGATGGAGAAATTATGGAGATAACTGA
GCAGAAAGGTGAGATTTTTTGAGTAAAACCTTGAATTTTGCATAAAAAATTG
CAATTTTCGCTAAAAATTACCTTAAAACCTCGAAAATTGGAATTTCTAGCTGAG
AAAATGGCCAAAAATGTCGAAAAATGCCTCCGAAACCTGTGAAAAAAAAAAA
CCACCAAAAAGGTTTCTAGGCCACCAAAAAGATTCTAGGCCACCAAAAATG
TTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACC
AAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAACAGGTTTCA
ATGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCCCCAAAA
AATTTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGC
CACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAGGT
TTCTAGGCCACCAACCAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCA
AAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTA

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FIGURE 27

GGCCACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAA
TGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAGGTTTCTAGGCC
ACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTT
TCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCA
AACAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAACAGGTTTCAA
TGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAA
TGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCA
CCAAACAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAACAGGTTT
CAATGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCCCCAA
AAAATTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAG
GCCACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAG
GTTTCTAGGCCACCAACCAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCAC
CAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTC
TAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAAGGTTTCAAGGCCACCAAA
AAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAACAGGTTTCAATG
CCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGG
TTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAGGTTTCTAGGCCAC
CAAACAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTC
TAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAA
AAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAATGTTTCTAGG
CCACCAAAACAGGTTTCAATGCCCCCAAAAATTTTCTAGGCCACCAAAAAG
GTTTCTAGGCCATCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCAC
CAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTC
TAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAA
AAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAGGTTTCTAGG
CCACCAACCAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAAAGG
TTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACC
AAAAAGGTTTCTAGGCCACCAAAAAGGTTTCAAGGCCACCAAAAAGGTTTCA
ATGCCACCAAAAATGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAA
AGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAGGTTTCTAGAC
CACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAGGT
TTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACC
AAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCT
AGGCCACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAA
ATGTTTCTAGGCCACCAAAACAGGTTTCAATGCCCCCAAAAATTTTCTAGGC
CACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGT
TTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACC
AAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCA
ATGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCCCCAAAA
AATTTTCTAGGCCACCAAAAAGGTTTCAATGCCACCAAAAATGTTTCTAGGC
CACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGT
TTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACC
AAAAATGTTTCTAGGCCACCAAAACAGGTTTCAATGCCACCAAAAAGGTTTCT
AGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAC
AGGTTTCAATGCCACCAAAAAGGTTTCTAGGCCACCAAAACAGGTTTCAATGC
CACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGT
TTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACC
AAACAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAACAGGTTTCA

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FIGURE 27

ATGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCCCCAAAA
AATTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGAC
CACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGACCACCAAAAAGGT
TTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACC
AAAAATGCTTCTAGGCCACCAAAAATGTTTCTACGCCACCAAAAAGCCGCCTC
AAGCCCGAAAAATTTGAATTTCCCGCTCAAAAAATCTAAAATTTTCCGATTTT
CAGACGAATCAGATGATGTGGTGATGCTGGACGACGATGATGACGACACTCC
GGAACCGATTCTCGTGATTGATATGGATGAGGATGAGGATGTTACTACAGAT
GGTCTGAATCTCAGGAAGAGCTGGCTGCAGATGCTCCGGCTCCAGGAGCTC
CAGAAGCTTCAGCTCCAGCTCAAGAAGCCTCAGAAGCTTCAGCTCCGGATCA
AGAAGCTCCAGAAGTTCAGGATGTTCCGGATTCTTCGGGAGCTCCAGATGCT
TCAGCTCAGGCTTCAGAGGCTTCTGATGCTTCAGCTCCAGAAGTTCAGGATC
TACAGAAGCTCAGGATGCTCAGGATGTTCCGGATTCTTTGGGAGCTTCAGAT
GCTTCAGCTCAAGAAATTCAGAAGCTCCAGAAGCCCCAGAAGCTCCAGAAA
TCGCCGCTGAAATCGACGAAGAAGTGCTGCTCGCCGAGCAAAAATGGAGTTTT
GGACGAAGGATTTGATGAGACTGACGATATTATCATAGAAGAAGAAGCTGTA
GAAGAAGCTGAAGCCGTGGAGCCACCAATTAACACTGAAAATCAGGAAAAC
GCGCTGGAAATGCTCGAAGAGCGCCTCAAGAAGAATGAAGAAAAGGAAATT
GTGGAGAAAAGTGATGTGAAGCCAGAGGATGAAGATATTATACATATGGAG
ACGGATTCAAGTTGAAAGTATGGGCTTTTTTAGCTGGAAAACAGGAAAAAAGA
GCAAAAAATTGATACATTTCCAGCTTAACCAATCTTTTTTTGAGTTGTAAAGC
CTGAAAATTGAGATTTTTGTACCAACTTTTATGATAAAGCTGAAAAAAAATT
AATTTTTTGACGAATTTTTAGCGGAAACCCTGAAAACATGTTTTGTCTGAAAA
ATACAGAAAATCGTCACTTTTTACAATAAATTCGAGATTTTTAGCTCAAAAAT
ACAACATTATAGTGCAAAAATCTCAGAAAAAGCCAAAAATTTCAATCAACA
TCTCAAAAAAAGCAGAAAATTTACTCAAAATATCTCAGAAAAAGCTAAAATT
TTCCCAAAAAATCCCAGAAAAAGCAGAATTTTCATTCAAAATTTCCAGAAAA
AGCTGATAATTTACTAAACAATCTCAGAAAAATGCTGAAATTTTACTCAAAAG
TCTTCATAAAAAGCTGAAATTTTACTTTAAAAGTTTAGGAAATGCTGCAATTT
CACTTAAAAATCCCAAAAAAGCTAAAATTTTCCCAAAAAATCCCAGAAAAAG
CAGAAATTTTACTCGAATATCTCAAAAAAAGCTGAAATTTCACTCAA
AAATCCCAGAAAAAGCTAAAAATTTACTAAAAAATCTCAAAAAAAGCTGAAATTTCACTCAA
CTAAAATTTCACTCAAAAATCTCAGAAAAAGCTAAAATTTTACTCGAATATCT
CAAAAAAAGCTGAAATTTTCTAAAAAATTTATGAAAAACCGAAATTTT
ACTTAAAAGTCTCATAAAAAGCCGAATTTTCCCAAAAAAATCCCAGAAAAAG
CTAAAAATTTACTTTAAAATCTCATCTGTAATTTTAGTTTAAAATCTCAGAAA
AACCCGAAATTTCTCTCAAAAATTTGCTGATTTTCAAATTTTCAAGCTCAAGC
CGCAAACGTACTGGCGGAGCCACAAGTCCGCGGAGCCCGGCTCAAAAACGA
CCAAAACGACGTGTTCAAACGTTATTAAAGATGCGTCAGAATGCAATTGAAC
TATTGACACGACTTTATGGCTCATGGGATGCACAATTGAGCCTCTCAAATCTT
GAGACAATTCGATTGTTGGGTGTCAATAATAAGGAAGCTTATCGAAATTTT
TGAGGAGAATGAGCAAGGTTAAAGCGTTTTTAAATGCTATGAAAACCTGACAA
ATTTTCGATAAAAAAAGGATTTTTGGAAGAAAATCGCCTGAAAATTCATGT
TTTTCTGCAAATTTTGACCAAATTTCCCAAGAAAAATACGATTTTTTAGTCCGA
AAATCCTCCAAAAAGATTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAG
AAAGTTTCTAGGCCACCAAAAGTATTTATAGGCCACCTAAGATGTTTCTAGGCC
ACCTGAGATGTTTCTAGGTCACCAAAAATGTTTCTCGGTCACCAAAAATGTTT
CAAGGCCACCGAAAAGGTTTCTAGGCCACCTAAGTATTTCTAGGCCACCTAA

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FIGURE 27

GATGTTTCTAGGCCACCTGAGATGTTTCTAGGTCACCAAAAATGTTTCTAGGT
TACCAAAAATGTTTCAAGGCCATCGAAAAGGTTTCTAGGCCACCAAAGTATT
TCTAGGCCACCTAAGATGTTTCTAGGCCACCTGAGATGTTTCTAGGTCACCAA
AAATGTTTCAAGGCCACCGAAAAGGTTTCTAGGCCACCAAAAAGGTTTCTAG
GCCACCAAAAATATTTCTAGGCCACCTAAGATGTTTCTAGGCCACCTGAGAT
GTTTCTAGGCCACCTGAGATGTTTCTAGGCCACCTGAGATGTTTCTAGGTCAC
CAAAAATGTTTCTCGGTCACCAAAAATGTTTCAAGGCCACCGAAAAGGTTTCT
TAGGCCACCTAAGTATTTCTAGGCCACCTAAGATGTTTCTAGGCCACCTGAGA
TGTTTCTAGGTCACCAAAAATGTTTCTAGGTTACCAAAAATGTTTCAAGGCCA
TCGAAAAGGTTTCTAGGCCACCAAAGTATTTCTAGGCCACCTAAGATGTTTCT
AGGCCACCTGAGATGTTTCTAGGTCACCAAAAATGTTTCAAGGCCACCGAAA
AGGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATATTTCTAGGC
CACCAAAAATGTTTCTAGGTCACCAAAAATGTTTCTAGGTCACCAAAAATGT
ATCAAGGCCACCAAAAAGGTTTCTAGGTCACCAAAAATGTTTCTAGGCCACC
AAAAATGTTTCTAGGTCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCT
AGGCCACCAAAAAGGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAA
AGGTTTCAAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGGT
CACCAAAAATGTTTCTAGGCCACCAAAGTATTTCTAGGCCACCTAAAAGGTTT
CTAGGCCATCAAAAAGGTTTCTAGGCCATCAAAAAGGATTCTAGGCCACCAA
AAATATTTCTAGGCCACCTAAGATGTTTCTAGGCCACCAGAGTATTTCTAGGC
CACCTAAGAGGTTTCTGGGCCATCAAAAAGGTTTCAAGTCCATCAAAAAGGT
TTCTAGGCCACCAAAAAGGTTTCTAGGCCACCGAAAAGGTTTCTAGGCCACC
AAAAAGGTTTCTAGACCACCTAAGACATTTCTAGGCCAACAAAAAGGTTTCT
AGGCCACCAAGAAAGCCGAAAAAAGTGTCTCAAATTCGAATTTTGCAGTGCTCA
AACAAAAAGTGTCGCACTGACAGAAGAGCTGAAAAAGGAGAAGCTGGCTC
ACGCGGGAACCCGTTTCAGCATTGAAAGAATTGACTAATGAAATAACTGGAAT
GCGTGTACAAATGAATAAACTACGTTCAATGGTCACTCAGCCTACGACTTCG
AAAATTATTGATAGTTTTGTTCAACGTCATCAGGCTTTCGAGCAGCAACAACA
ATTCCAACACCAACACCACCAACACCGACCAATAATGTTGGCTCCACGTCAT
CATCCGCCGCCGCCCGCCGATTTTACACCGAATCAACGGGCGGCGGCTCCGT
ATCATCCGAATATGGTTCAACCGAATCGTCTTGCTGCTATGCCACATAGAAGA
CCGATTATTGGAATGCAGGTGAAAATGGAATGCCATGAAAATTTCCGGCCCGG
AAAATTTTGAAAAATCCTCTAAATTTTCAATATTTGTGCAAAAAATCTGACAA
AAATCGTGTCAAAATTCAGATTTCCGGGAGAAAAATCGCATTTTGTAGTAAA
AATTTCGAAGAAAAGCGTCTTAAATTCTAGATTTATTAGTTAAAAATTTTTTCA
AATTTTAGTCAAGAAAATTAAGAAAAATGCGAAAATTTTCGAGCAAAAAATAT
AGTTTTTTGGAGCCGAAATTGTGAAAAATGCGATTTTTTTTCGAAAAATCTGGA
CAAAAAATTTCAAACAAGAAAAACCACTTTTTTAAAAAAATTTTCACACAAT
TTCCAGCAACAAAATTCGGCTCCACCACAATTCAACGGTCACCAAGCTCTCGT
CCCATCACCTCAATCATCTGCATTTTCTCGTCCACCACCAACTCAACTTG
CAACACAGAGAAGAGCTCCACCATTGGCAAGTACCGGCCTTCCGGCAACAGT
CAGATGGGAAGCAATTCACCGCCAAAAAATCCGAATGTCGGGCACAATGA
GCCACCGCTTAACAATGGAGGTTTCGTGCTGTGCAACAAAAAGAGCACCGCTT
TTCCACGACGAGTTTTTTCGATGATGATTTTGGTGTGAAAATTGAAAAACTCA
TTTTTTTAAAGTCTGAAATTTGAAAATTTGAGAAAAGTTTTTAAAAAAAGTT
TTATGAGGGATTTTCTGACAATTTTTTATAAACGGAAAATTACGAAAACCTCCA
AAATTTGTGTTCTTTTCGGAAAACGAATTTGAAATTTGAACCAAAATTTTGACA
ATTTTCTGGGGATTTTTGACTGGAAATTCGTTTTTCATCGATTTTTCCTCCTTT

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FIGURE 27

AATTTTCGGTAAAACCCCTGTCTCCAATTCCAGGCCGTGCACAGCCACTAATC
GATAATACACGTGTACACGACAATACAATTATGCTGTGTGTACCACTTGTCTC
CACTGCAAATACAATATCATCGGGCGATTTCGACACGTCTACCAAAAGTACCA
CGAATCTACGAGAATCTCACGGCAAATCCCGATTGAGTGTGACGATTCATTC
GAGTGCACAGGATTTCCGAGAGAATTATCAAATTGGTGGAAAGATTAACTAT
GAATATCTCGGAGGATTTGATCAATATGTAGGTGATGATGTTTTTTTTATTGAG
AGATAAATACGAAATTCCATTACAATCGATATTTTTTGACTGAAAAATGTCTG
AAAAATCAAAAATTTTAGCTAAAAATTGAGAATATTTTTGTTTAAAAAAAT
CATTGAAATTGATTTTTTTTTATTCCATAAAAAATCTCGGAAAAGTCAATTTTC
AGTCATAAATCTTCTGAAAATTATCCAAACAATGGGATTTTCTGAAATTTTAG
CTTAAAAATTGAGGATTTCCCGGTTTTTTCAGAGAAATTCCATTACAATCGAT
TTTTTTACTGAAAAATCCTCTGGAAATTAACAAAAACCAAATAAAAATGCCCT
AATTTTTTTTTTAAATCCAAAAATTGTTGGATTTTTTTCAGAAAAAAATATTTTTT
CAATTGACTGGTGTCCAAAAAATATAGAAAATTCAAATTTTCCAAGAAAAAT
AGCCAAAAAAATGTAATTTTTGTCTAACAAAAAAATTGAATAGCGCAAAATT
AAATTGTCGTTTTTTTTAATTTCCCTCCGGTTTTGAAAGGAAAAAATTCCATA
AAAATCGAAATTTTTTGACTGAAAAATCCATGAAAACCTCGAATTTTGAGTCA
AAAATCCTCTGAAAATGCTCCAAAATATGAGATTTTCTGAAATTTTCATCAAAA
ATTAAGAATTTACGGTTTAAAAAAAATTCCATTAAAATCGATATTTTTCAAG
TGAAAAATCTCTGGAAAACCTCGATGTTTGAGTCAAAATTCGTCTGAAAATGC
TCCTTTAAATTGAAAAATTGAAAAAAAACCGCCCAACAATATTTGCAGAATA
TCCAAGTGTTCTGTTCAAGTGTCTCTTAAATTCAGTGAATGAACGGTTAC
CCGGATCCAGAAGATCGTATATCAATTGACTGGGGATGCTCGAAATTGTGGC
CTTGTAAGCCGAAATCTCATCACAATTCCGTGTACGCTTCCATCAAGCACAA
CTGCTGCCGAAGAACGATCGAATTACGATTGTGGCTGTGGCGAAGGATAAAA
CTAGCGGAATTATTCACATTTTCGCAGGTGAAAAATTGGAAAATTTGCACAAA
TCCAGACAAAAAAACTGAAAAATCGAAAAAATTTTTGTAATTTTTTGCCGA
AAACGAAAATTAAAAACTGATAAAAATTGATTTTTTAACCGGAAAATCCCTGA
AAAATCAAACATTTTTTGCTAAAAATTGAGAATTATACGGTTTTGGGTAAAA
AAAAACTATTTAAAAAAAATATTTTTTCTTTAAAAATCTCAACAAAAAAA
ACCAATTTTCATTTCAGAAATCCCCCGGAGAATTGTCAAAATTTTGGGAATAC
TCTGAAATTTTCGATAAACACCTCATTTTTGATTAAATGATTTTTTTAACTGA
AAAATCCCTTAAAAAACGAATATTTTAGTTTTTTCACAAAAAAATGTGCAATT
TATCTGAAATTTTCAGCAAAAAAAATGAAAAAAAATTCGGAAATTAAAA
ACTGATAAAAATCGATTTTTTACTTGAAAAATTCGTGAAAAATCAAACACATT
TTTGCTAACCATTTGAGAATATTACGATTTTGTGAAAAAAAACCATTA AAA
TTGATTTTTTATTCTTAAAAAATGCCAGAAAAATCAATTTTCAGTCAAAAATC
ACCGGAAAATTATCAAAATTTTGAGGTTTTCTGTGAAATTTCAAGCTGAAATT
TCCATTTTTGAATAAAAAAAATGTGGCTGGATTTAAAAAAAACCATTA AAA
TTGATTTTTTAACTGAAAAATCCGTATTTCTCTGAAATTTTCAGGCAAAAAATG
TCATTTCCGAAATTAAAAATTGCGACAAAATCAAATAAAATTGATCAAAATTT
GCAAAAAAAAACCTTTTCGCAAAAAATCCTTAAAATTTACATTTTTCAAC
AAAAACTCGAATTTTCAGTCAAAAATTCGTCTGAAAATGCTCCAAAATATGG
GATTTTTTGAATTTTAGCTAAAAATTGAGAATTGCACGGTATTTAGAGAGGG
AAAAATTCATAAAAAATCGATATTTTCTTAAAAATCTCGAAAAAATCAT
CAATTTTCATTCAAAAATCCCCCGGAAAATTGTCAAAATTTTGAGATTTTT
CTGAAATTTACGCAAAAATTTTCATTTTTTTCAGCCACCTTCATCACTCTCGA
ATGATCGATCTCTTCACGTCAAATGCACTTTTTTCTGGATTTTTTTGTAAAAA

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FIGURE 27

ATTTGAAATTCTCGTGTTTTTCTTCTGAAAAATTGCTTTTTTTGATTTTTCTG
TAATTTTTTTTTGTTGATTTTCTTAATTTTTTAATTTTCAAAAAATCTTTTC
ATCTCTTCTCTCTCTCTCTGAATCTCAATTTTTTCTGAATTTCCCGTTTTT
TCTGATAATTTTCAATATTTCTCTGAATTTTCTATTCCCCCGTTGTAATGCC
AAAATATGTGGTAATTTCTCCCCATTTTTTCGCTTTATTACTATTTATTCTATT
CAATTGGTGCCTCTCTCAATGTGTTGTATGAAAAACACTGTTTTATGGAGGTT
TTGGAGAATTTTGAATTTTTTCGTCTGATTTTTATTGGTTTTCTTTACCAATT
CAATTTTTTTTTTAATTCGAAAATTTGTAGAAATTCATTTTGTAGCTTAAAAA
ATTAAAAATTGAGAAAATTTGTTCAAAAATGGCAAAGTTTTCGAAATTTTAGT
CTAAAAAAGATTTTTTTAATATAGAATTTTAAAAAATTAGCACAGAAAAAT
GCCGAAAAATTCGTAATTTTTTCATTTAAAAATGAAAAAAAAAAAAACAAAA
AAAAAAAAAAAAAAGAGGGGAAAAATCCCATTAAGTAGTTTTTTGACTGC
AAAATCGTCTGGAAATTAACAAAATTTAAAAAATCTTTTTTACAGCCCATCG
TTTCCAAAAACCAATAAAATGCCAAAAAATTTTATGCAAAAATTCTG
GATTTTTTCCGATTTTTTCAAAAAATTCCTTCTAAAAAATGGTGAAT
TTGTTCCCAAAAACCAAAATTTGAGATTTTCTAAAATTTTGGCAAAAATTAA
GAATTCACGGTTTTGAGAGGGGAAAACTCCATTAATTTGATGATTTTATGA
CTAAAAATTCCTAAAAATCAATTTTCAGTCAAAAATTAAATTT

Figure 28

MSEVIDESILNTEASDDPIPPLNDDQIAELLGEDGEIMEITEQKDESDDVVMLDDD
DDDTPEPILVIDMDEDEDVTTDGPESQEELAADAPAPGAPEASAPAEASEASAP
DQEAPEVQDVPDSSGAPDASAQASEASDASAPEVPGSTEAQDAQDVPDSLGS
ASAQEIPEAPEAPEAPEIAAEIDEEVLLAEQNGVLDEGFDETDDIIIEEEAVEEAEA
VEPPINTENQENALEMLEERLKKNEEKEIVEKSDVKPEDEDIIHMETDSVETSSRK
RTGGATSPRSPAQKRPKRRVQTLLKMRQNAIELLTRLYGSWDAQLSLSNLETIRL
LGVNNNRKLIEFEENEQVLKQKVSALTEELKKEKLAHAGTRSALKELTNEITGM
RVQMKNKLRSMTQPTTSKIISFVQRHQAFEQQQQFQHQHHQHRPIMLAPRHP
PPPHFTPNQRAAAPYHPNMVQPNRLAAMPHRRPIIGMQQQNSAPPQFNHQAAL
VPSPQSSSAFSRPPPTQLATQRRAPPLASTGLPATVRWEAIPPKNPVGHNEPPL
NNGGRAQPLIDNTRVHDNTIMLCVPLVSTANTISSGDSTRLPKVPRIYENLTANPD
LSVTIHSSAQDFRENYQIGGKINYEYLGGFQYNIQVFVQVSSLKFTGMNGYPDP
EDRISIDWGCSKLWPCKPKSHHKFRVRFHQAQLLPKNDRITIVAVAKDKTSGIIHI
SQPTFITLE

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Figure 29

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1 aaggaattag actctttatc taaagtgaag aatgatcaat taagaagttt ttgtcccata
61 gaattaaata taaatggatc tcttggggca gaatctgatt tggcaacatt ttgcacttct
121 aaaactgatg ctgttttaat gacttctgat gatagtgtga ctggatcgga attatcccct
181 ttggtcaaag catgcatgct ttcatacaat ggatttcaga atattagtag gtgcaaagaa
241 aaagacttgg atgataacctg catgctgcat aagaagtcag aaagccatt tagagaaaca
301 gaacctctgg tgtcaccaca ccaagataaa ctcagtctta tgccagttat gactgtggat
361 tattccaaaa cagtagttaa agaaccagtt gatcacgagg tttcttgctg caaaacaaaa
421 gattcagaca tatactgtac tttgaacgat agcaaccctt ctttgtgtaa ctctgaagct
481 gaaaatattg agccttcagt tatgaagatt tcttcaaata gctttatgaa tgtgcatttg
541 gaatcaaaac cagttatatg tgatagtaga aatttgacag atcactcaaa atttgcattg
601 gaagaatata agcagagcat cggtagcact agttcagctt ctgttaatca ttttgatgat
661 ttatatcaac ctattgggag ttcaggtatt gcttcattct ttcagagtct tccaccagga
721 ataaaggtgg acagtctaac tctcttgaaa tgcggagaga acacatctcc agttctggat
781 gcagtgctaa agagtaaaaa aagttcagag tttttaaagc atgcagggaa agaaacaata
841 gtagaagtag gtagtgacct tcttgattca ggaaagggat ttgcttccag ggagaacagg
901 cgtaataatg ggttatctgg gaaatgtttg caagaggctc aagaagaagg gaattccata
961 ttgcctgaaa gaagaggaag accagaaatc tctttagatg aaagaggaga aggaggacat
1021 gtgcatactt ctgatgactc agaagttgta ttttcttctt gtgatttgaa ttaaccatg
1081 gaagacagtg atggtgtaac ttatgcatta aagtgtgaca gtagtgggtc tgccccagaa
1141 atttgttcta cagttcatga agattattct ggctcttctg aaagttcaaa tgatgaaagt
1201 gattcagaag atacagattc ggatgatagc agtattccaa gaaaccgtct ccagtctgtt
1261 gtggttgatg caaagaattc tactttgccc atggaagaaa caagtccttg ttcttctcgg
1321 agcagtcaaa gttatagaca ctattctgac cattgggaag atgagagatt ggagtcaagg
1381 agacatttgt atgaggaaaa atttgaaagt atagcaagta aagcctgtcc tcaaactgat
1441 aagtttttcc ttcataaagg aacagagaag aatccggaag tttcttttac acagtcagat
1501 agaaaaaaaa tagataaccg cctgcctgaa ctttctcatc ctcagagtga tggggttgat
1561 agtacaagtc atacagatgt gaaactctgac cctctgggtc acccaaattc agagaaaacc
1621 gtgaaagcca aaataccttc taggcagcaa gaagagctgc caatttatc ttctgatttt
1681 gaagatgtcc caaataagtc ttggcaacag accactttcc aaaacaggcc agatagtaga
1741 ctgggaaaaa cagaattgag tttttcttcc tcttgtaga taccacatgt ggatggcttg
1801 cactcatcag aagagctcag aaacttaggt tgggacttct ctcaagaaaa gccttctacc
1861 acgtatcagc aacctgacag tagctatgga gcttggtgtg gacacaagta tcagaaaaat
1921 gcagaacagt atggtgggac acgtgattac tggcaaggca atggttactg ggatccaaga
1981 tcaggtagac ctcctggaac tggggttggt tatgatcgaa ctcaaggaca agtaccagat
2041 tccctaacag atgatcgtga agaagaggag aattgggatc aacaggatgg atccccattt
2101 tcagaccagt ccgataaatt tcttctatcc cttcagaaag acaaggggtc agtgcaagca
2161 cctgaaataa gcagcaattc cattaaggac actttagctg tgaatgaaaa gaaagatttt
2221 tcaaaaaact tagaaaaaaa tgatatcaaa gatagagggc ctcttaaaaa aaggaggcag
2281 gaaatagaga gtgattctga aagtgatggt gagcttcagg acagaaagaa agttagagtg
2341 gaggtagagc agggagagac atcagtgcc ccaggttcag cactggttgg gccctctgt
2401 gtcattgatg acttcaggga cccacagcga tggaaaggaat gtgccaagca agggaaaatg
2461 ccattgttact ttgatcttat tgaagaaaat gttattttaa cagaaagaaa gaagaataaa
2521 tctcatcgag atattaagcg aatgcagtgt gagtgtacac ctctttctaa agatgaaaga
2581 gctcaagggtg aaatagcatg tggggaagat tgtcttaate gtcttctcat gattgaatgt
2641 tcttctcggt gtccaaatgg ggattattgt tccaatagac ggtttcagag aaaacagcat
2701 gcagatgtgg aagtcatact cacagaaaag aaaggctggg gcttgagagc tgccaaagac
2761 cttccttcga acacctttgt cctagaatat tgtggagagg tactcgatca taaagagttt
2821 aaagctcgag tgaaggagta tgcacgaaac aaaaacatcc attactattt catggccctg
2881 aagaatgatg agataataga tgccactcaa aaaggaaatt gctctcgttt catgaatcac
2941 agctgtgaac caaattgtga aacccaaaaa tggactgtga acggacaact gaggggttggg
3001 ttttttacca ccaaactggg tcttccaggc tcagagttaa cgtttgacta tcagttccag
3061 agatatggaa aagaagccca gaaatgtttc tgcggatcag ccaattgccg ggggtacctg
3121 ggaggagaaa acagagtcag catcagagca gcaggaggga aaatgaagaa ggaacgatct
3181 cgtaagaagg attcagtgga tggagagcta gaagctctga tggaaaatgg tgagggtctc
3241 tctgataaaa accaggtgct cagcttatcc cggctaattg ttagaattga aactttggag

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FIGURE 29

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3301 cagaaactta cctgtctgga actcatacag aacacacact cacagtcctg cctgaagtcc
3361 tttctggaac gtcattgggt gtctttgttg tggatctgga tggcagagct aggtgacggc
3421 cgggaaagta accagaagct tcaggaagag attataaaga ctttggaaca cttgccatt
3481 cctactaaaa atatgttgga ggaaagcaaa gtacttccaa ttattcaacg ctggtctcag
3541 actaagactg ctgtccctcc gttgagtga ggagatgggt attctagtga gaatacatcg
3601 cgtgctcata caccactcaa cacacctgat ccttccacca agctgagcac agaagctgac
3661 acagacactc ccaagaaact aatgtttcgc agactgaaaa ttataagtga aaatagcatg
3721 gacagtgcaa tctctgatgc aaccagtga ctagaaggca aggatggcaa agaggatctt
3781 gatcaattag aaaatgtccc tgtagaggaa gaggaagaat tgcagtcaca acagctactc
3841 ccacaacagc tgcctgaatg caaagttgat agtgaaacca acatagaagc tagtaagcta
3901 cctacatctg aaccagaagc tgacgtgaa atagagctca aagagagcaa cggcacaaaa
3961 ctagaagaac ctattaatga agaaacacca tccaagatg aagaggaggg tgtgtctgat
4021 gtggagagtg aaaggagcca agaacagcca gataaaacag tggatataag tgatttggcc
4081 accaaaactcc tggacagttg gaaagacctt aaggagggtat atcgaattcc aaagaaaagt
4141 caaactgaaa aggaaaacac aacaactgaa cgaggaaggg atgctgttgg cttcagagat
4201 caaacacctg ccccgaagac tcctaatagg tcaagagaga gagaccaga caagcaaact
4261 caaaaataag agaaaaggaa acgaagaagc tccctctcac caccctcttc tgcctatgag
4321 cggggaacaa aaaggccaga tgacagatat gatacaccaa cttctaaaaa gaaagtacga
4381 attaaagacc gcaataaact ttctacagag gaacgccgga agttgtttga gcaagagggtg
4441 gctcaacggg aggtcagaa acaacagcaa cagatgcaga acctgggaat gacatcacca
4501 ctgccctatg actctcttgg ttataatgcc ccgcatcatc cctttgctgg ttaccacca
4561 ggttatccca tgcaggcta tgtggatccc agcaacccta atgctggaaa ggtgtcctg
4621 cccacacca gcatggacc agtgtgttct cctgtcctt atgatcatgc tcagcccttg
4681 gtgggacatt ctacagaacc cctttctgcc catccaccag taccagtgtg gccacatgtg
4741 gcagctcctg tggaaagttc cagttccag tatgtggccc agagtgtgg tgtagtacac
4801 caagactcca gcgttgctgt cttgccagt cgggccccc gcccagttca gggacagaat
4861 tatagtgttt gggattcaaa ccaacagtct gtcagtgtac agcagcagta ctctcctgca
4921 cagtctcaag caaccatata ttatcaagga cagacatgtc caacagtcta tgggtgtgaca
4981 tcaccttatt cacagacaac tccaccaatt gtacagagtt atgccagcc aagtcttcag
5041 tatatccagg ggcaacagat ttacacagct catccacaag gagtgggtgt acagccagcc
5101 gcagcagtga ctacaatagt tgcaccaggg cagcctcagc ccttgagcc atctgaaatg
5161 gttgtgacaa ataatctctt ggatctgccg cccccctctc ctcccaaacc aaaaaccatt
5221 gtcttacctc ccaactggaa gacagctcga gatccagaag ggaagattta ttactaccat
5281 gtgatcacia ggcagactca gtgggatcct cctacttggg aaagcccagg agatgatgcc
5341 agccttgagc atgaagctga gatggacctg ggaactccaa catatgatga aaaccccatg
5401 aaggcctcga aaaagcccaa gacagcagaa gcagacacct ccagtgaact agcaaagaaa
5461 agcaaagaag tattcagaaa agagatgtcc cagttcatcg tccagtgcct gaacccttac
5521 cgaaaacctg actgcaaagt gggaagaatt accacaactg aagactttaa acatctggct
5581 cgcaagctga ctacgggtgt tatgaataag gagctgaagt actgtaagaa tcttgaggac
5641 ctggagtga atgagaatgt gaaacacaaa accaaggagt acattaagaa gtacatgcag
5701 aagtttgggg ctgtttacaa acccaaagag gacactgaat tagagtgact gttgggcccag
5761 ggtgggagga tgggtggtca ggtaagacag actctagggg gaggaatcc tgtgggccc
5821 tctgtccac ccctgtcagc actgtgtctac tcatgataca tcaccctggg gaattcaacc
5881 ctgcagatgt caactgaagg ccacaaaat gaactccatc tacaagtgat tacctagtgtg
5941 tgagctgttg gcatgtggtt agaagccatc agaggtgcaa gggcttagaa aagaccctgg
6001 ccagacctga ctccactctt aaacctgggt cttctccttg gcggtgtgt cagcgcacag
6061 acccatgcgc atccccaccc acaacctttt accctgatga tctgtattat attttaatgt
6121 atatgtgaat atattgaaaa taatttgttt tttcctggtt tttgtttggt tttcgttttg
6181 cttttagcct ctacatgcta ggatcacagg aagactttgt aaggacagtt taagttctcc
6241 tgcaagggtt aatttgttat catgtaaaata ttccaaagca ggctgccttg tggttttggc
6301 cagccttggt ctatgttgat aagattgatt tactgttaa aatcacttta ctttatccaa
6361 tttttactga actttttatg taaaaaata aatcaatta aag

```

Figure 30

KELDSLKVKNDQLRSFCPIELNINGSPGAESDLATFCTSKTDAVLMTSDDSVTGSELSPLVKACMLSSNG
FQNI SRCKEKDLDDTCMLHKKSESPFRETEPLVSPHQDKLMSMPVMTVDYSKTVVKEPVDTRVSCCKTKDS
DIYCTLNDSNPISLCNSEAENIEPSVMKISSNSFMNVHLESKPVICDSRNLT DHSKFACEEYKQSIGSTSSA
SVNHFDLYQPIGSSGIASSLQSLPPGIKVDLSLTLKCGENTSPVLDAVLKSKKSSEFLKHAGKETIVEVG
SDLPDSGKGFASRENNRNNGLSGKCLQEAQEENSLPERRGRPEISLDERGEGGHVHTSDDSEVVFSSCD
LNLTMEDSDGVTYALKCDSSGHAPEIVSTVHEDYSGSSESSNDESSEDTSDDSSI PRNRLQSVVVVPKN
STLPMEETSPCSSRSSQSYRHSDHWEDERLESRRHLYEEKFESIASKACPQTDKFFLHKGTEKNPEISFT
QSSRKQIDNRLPELSHPQSDGVDSTSHTDVKSDDLPHNPSEETVKAKIPSRQQEELPIYSSDFEDVFNKSW
QQTTFQNRPD SRLGKTELSFSSSCEIPHVDGLHSSEELRNLGWDFSQEK PSTTYQQPDSSYGACGGHKYQQ
NAEQYGGTRDYWQNGYWDPRSGRPPGTGVVYDRTOGQVPDSLTDREEEENWDQQDGSFSDQSDKFLLS
LQDKGVSQAPEISSNSIKDTLAVNEKKDFSKNLEKNDIKDRGPLKKRRQEIESDSESDELQDRKKVRVE
VEQGETSVPPGSALVGPSCVMDDFRDPQRWKECAKQGMPCYFDLIEENVYLTERKKNKSHRDIKRMQCEC
TPLSKDERAQGEIACGEDCLNRLLMIECSSRCPNGDYCSNRRFQRKHADVEVILTEKKGWGLRAAKDLPS
NTFVLEYCGEVL DHKEFKARVKEYARNKNIHYYFMALKNDEIIDATQKGNCSR FMNHSCEPNCETQKWTVN
GQLRVGFFTTKLVPSSGSELTFDYQFQRYGKEAQKCFGSANCRGYLGGENRVSI RAAGGKMKKERSRKDS
VDGELEALMENEGELSDKNQVLSLSRLMVRIETLEQKLTCLLELIQNTHSQSCLKSFLERHGLSLLWIWMAE
LGDGRESNQKLQEEIIKTLEHLPIPTKNMLEESKVLPIIQRWSQTKTAVPPLSEGDGYSENTSRAHTPLN
TPDPSTKLSTEADTDTPKKLMFRRLKIISENSMDSAISDATSELEGKDGEDLDQLENV PVEEEELQSQQ
LLPQQQLPECKVDSETNIEASKLPTSEPEADAEIELKESNGTKLEEPINEETPSQDEEEGVSDVESERSQEQ
PDKTVDISDLATKLLDSWKDLKEVYRI PKKSQTEKENTTTERGRDAVGFRDQTPAPKTPNRSRERDPDKQT
QNKEKRKRSSSLSPSSAYERGTRPDDRYDTPTS KKKVRIKDRNKLSTEERRKLFEEQAQREAAQKQQQQ
MQNLGMTSPLPYDSLGYNAPHHPFAGYPPGYPMQAYVDPSPNPAGKVLLPTPSMDPVCSPAPYDHAQPLVG
HSTEPLSAPPPVPVPHVAAPVEVSSSYVAQSDGVVHQDSSVAVLPVPAPGPVQGGQNYSVWDSNQSVSV
QQQYSPAQSQATIIYYQGQTCPTVYGVTSPYSQTTPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAVT
TIVAPGQPQLQPEMVVTNNLLDLPPSPPKPKTIVLPPNWK TARDPEGKIYYYHVITRQTQWDPPTWES
PGDDASLEHEAEMDLGTPTYDENPMKASKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYRKPDCCK
VGRITTTEDFKHLARKLTHGVMNKELKYCKNPEDLECNENVKHKTKEYIKKYMQKFGAVYKPKEDTELE

Confidently predicted domains, repeats, motifs and features:

name	begin	end	E-value
<u>Pfam:AT_hook</u>	47	60	1.80E+01
<u>low complexity</u>	230	243	-
<u>low complexity</u>	327	338	-
<u>low complexity</u>	371	400	-
<u>low complexity</u>	505	530	-
<u>coiled coil</u>	549	621	-
<u>AWS</u>	636	682	8.80E-18
<u>SET</u>	683	811	6.00E-41
<u>PostSET</u>	812	828	7.40E-04
<u>low complexity</u>	1080	1093	-
<u>low complexity</u>	1118	1129	-
<u>low complexity</u>	1138	1158	-
<u>low complexity</u>	1271	1287	-
<u>VWV</u>	1361	1393	4.10E-08
<u>low complexity</u>	1447	1468	-
<u>low complexity</u>	1469	1497	-

These features and domains are not shown in the diagram, either because their scores are less significant than the required threshold, or because they overlap with some other source of annotation:

name	begin	end	E-value	reason
<u>low complexity</u>	36	50	-	overlap
<u>low complexity</u>	532	554	-	overlap
<u>low complexity</u>	569	615	-	overlap
<u>Pfam:SET</u>	677	811	8.80E-48	overlap
<u>low complexity</u>	734	739	-	overlap
<u>Pfam:VWV</u>	1362	1391	1.90E-08	overlap

Figure 31 LIN(n3628) Functional domains

Confidently predicted domains, repeats, motifs and features:

name	begin	end	E-value
<u>low complexity</u>	387	411	-
<u>low complexity</u>	435	449	-
<u>AWS</u>	845	900	7.50E-30
<u>SET</u>	901	1024	3.10E-41
<u>PostSET</u>	1025	1041	2.50E-05
<u>low complexity</u>	1262	1286	-
<u>low complexity</u>	1333	1344	-
<u>low complexity</u>	1425	1437	-
<u>coiled coil</u>	1468	1491	-
<u>low complexity</u>	1569	1589	-
<u>low complexity</u>	1605	1619	-
<u>low complexity</u>	1622	1643	-
<u>low complexity</u>	1690	1710	-
<u>VWV</u>	1741	1773	2.10E-11

These features and domains are not shown in the diagram, either because their scores are less significant than the required threshold, or because they overlap with some other source of annotation:

name	begin	end	E-value	reason
<u>Pfam:SET</u>	895	1024	6.30E-52	overlap
<u>low complexity</u>	1477	1493	-	overlap
<u>low complexity</u>	1726	1744	-	overlap
<u>Pfam:VWV</u>	1742	1771	6.90E-12	overlap

Figure 32 KIAA1732 Domains

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING

Applicant(s): Horvitz *et al.*

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